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OM protein - protein search, using sw model

Run on: January 9, 2006, 11:04:11 ; Search time 134 Seconds
(without alignments)
563.979 Million cell updates/sec

Title: US-09-461-646-4
Perfect score: 956
Sequence: 1 ALAAYRLEDTFGPDPTMIRA.........PGDNDIFESLYYRKMYGDMA 172
Scoring table: BLOSUM62
                Gapop 10.0 , Gapext 0.5
Searched: 2443163 seqs, 439378781 residues
Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%   Maximum Match 100%
Listing first 45 summaries

Database :   A_Geneseq_21:*
                1: geneseqp1980s:*
                2: geneseqp1990s:*
                3: geneseqp2000s:*
                4: geneseqp2001s:*
                5: geneseqp2002s:*
                6: geneseqp2003as:*
                7: geneseqp2003bs:*
                8: geneseqp2004s:*
                9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Match Length	DB	ID	Description
1	956	100.0	172	3	AAY92941	Aay92941 Human con
2	956	100.0	347	1	AAW12694	Aaw12694 Connectiv
3	956	100.0	348	5	ABB09204	Abb09204 Human ctg
4	956	100.0	349	2	AAR79964	Aar79964 Connectiv
5	956	100.0	349	2	AAW11302	Aaw11302 Connectiv
6	956	100.0	349	2	AAW09089	Aaw09089 Human con
7	956	100.0	349	2	AAW62084	Aaw62084 Human con
8	956	100.0	349	2	AAW81425	Aaw81425 Connectiv
9	956	100.0	349	2	AAY18361	Aay18361 Human con
10	956	100.0	349	2	AAY92939	Aay92939 Human con
11	956	100.0	349	3	AAY92940	Aay92940 Human con
12	956	100.0	349	3	AAY44755	Aay44755 Human con
13	956	100.0	349	3	AAB84598	Aab84598 Amino aci
14	956	100.0	349	4	AAB90791	Aab90791 Human she
15	956	100.0	349	4	AAB60664	Aab60664 Human con
16	956	100.0	349	4	AAB48831	Aab48831 Human con
17	956	100.0	349	4	AAE05923	Aae05923 Human con
18	956	100.0	349	5	ABP68624	Abp68624 Human pan
19	956	100.0	349	6	ABR92069	Abr92069 Human cer
20	956	100.0	349	6	ABR43135	Abr43135 Human con
21	956	100.0	349	6	ADA43043	Ada43043 Human con
22	956	100.0	349	6	ADB25763	Adb25763 Human con
23	956	100.0	349	6	ADB25761	Adb25761 Human con
24	956	100.0	349	6	ADB25765	Adb25765 Human con
25	956	100.0	349	6	ADB25764	Adb25764 Human con
26	956	100.0	349	7	ADB75254	Adb75254 Prostate
27	956	100.0	349	8	ADH10248	Adh10248 Human CTG
28	956	100.0	349	8	ADI27154	Adi27154 Human LRP
29	956	100.0	349	8	ADL82863	Adl82863 Human PRO
30	956	100.0	349	8	ADN04376	Adn04376 Antipsori
31	956	100.0	349	8	ADQ26762	Adq26762 Form proc
32	956	100.0	349	8	ADQ93890	Adq93890 Human con
33	956	100.0	349	8	ADR14059	Adr14059 Human NF-
34	956	100.0	349	8	ADV86252	Adv86252 Human con
35	956	100.0	349	9	ADY72449	Ady72449 Human con
36	956	100.0	349	9	ADY72447	Ady72447 Human con
37	956	100.0	349	9	ADY72445	Ady72445 Human con
38	956	100.0	349	9	ADY72448	Ady72448 Human con
39	956	100.0	349	9	ADZ21697	Adz21697 Human con
40	956	100.0	349	9	AEA00218	Aea00218 CTGF prot
41	938	98.1	349	9	ABR43136	Abr43136 Bovine co
42	937	98.0	349	6	ABR43137	Abr43137 Porcine c
43	934	97.7	347	2	AAY24379	Aay24379 Rat conne
44	934	97.7	347	2	ABR43138	Abr43138 Rat conne
45	934	97.7	347	8	ADH10252	Adh10252 Rat CTGF

ALIGNMENTS

RESULT 1
AAY92941

ID   AAY92941 standard; protein; 172 AA.
XX
AC   AAY92941;
XX
DT   08-NOV-2000 (first entry)
XX
DE   Human connective tissue growth factor protein fragment.
XX
KW   Human; connective tissue growth factor; CTGF; mitogen; antibody; liver;
KW   fibroproliferative disease; scleroderma; fibrosis; kidney; arthritis;
KW   hypertrophic scarring; atherosclerosis; diabetic nephropathy; retinopathy;
KW   hypertension; cardiovascular disorder; wound healing; bone repair.
XX
OS   Homo sapiens.
XX
PN   WO200035939-A2.
XX
PD   22-JUN-2000.
XX
PF   14-DEC-1999;   99WO-US029654.
XX
PR   14-DEC-1998;   98US-0112240P.
PR   14-DEC-1998;   98US-0112241P.
XX
PT   New fragment of connective tissue growth factor (CTGF) polypeptide having
PT   mitogenic activity, useful in wound healing, bone and tissue repair.
XX
PA   (UYMI-) UNIV MIAMI.
PA   (FIBR-) FIBROGEN INC.
XX
PI   Grotendorst GR, Neff TB;
XX
DR   WPI; 2000-431568/37.
DR   N-PSDB; AAA11281.
XX
PS   Disclosure; Fig 3; 71pp; English.
XX
CC   This sequence represents a fragment of the human connective tissue growth
CC   factor (CTGF) polypeptide which has mitogenic activity. The sequence
CC   covers the amino acids encoded by exons 4 and 5 of the full length cDNA
CC   sequence (AAA11280). The protein can be used to raise antibodies which
CC   specifically bind to CTGF and are used to treat a CTGF-associated disease
CC   or disorder, e.g. a fibroproliferative disease/disorder such as kidney
CC   fibrosis, scleroderma, pulmonary fibrosis, liver fibrosis, arthritis,
CC   hypertrophic scarring, atherosclerosis, diabetic nephropathy and

```
CC   retinopathy, hypertension, kidney disorders, angiogenesis-related
CC   disorders, skin fibrotic disorders, and cardiovascular disorders. The
CC   protein is also useful in wound healing, bone and tissue repair
XX
SQ   Sequence 172 AA;

Query Match             100.0%;  Score 956;  DB 3;  Length 172;
Best Local Similarity   100.0%;  Pred. No. 1.7e-85;
Matches 172;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Qy    1 ALAAYRLEDTFGPDPTMIRANCLVQTTEWSACSKTCGMGISTRVTNDNASCRLEKQSRLC 60
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Db    1 ALAAYRLEDTFGPDPTMIRANCLVQTTEWSACSKTCGMGISTRVTNDNASCRLEKQSRLC 60

Qy   61 MVRPCEADLEENIKKGKHKCIRTPKISKPIKFELSGCTSMKTYRAKFCGVCTDGRCCTPHR 120
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Db   61 MVRPCEADLEENIKKGKHKCIRTPKISKPIKFELSGCTSMKTYRAKFCGVCTDGRCCTPHR 120

Qy  121 TTTLPVEFKCPDGEVMKKNMMFIKTCACHYNCPGDNDIFESLYYRKMYGDMA 172
        |||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121 TTTLPVEFKCPDGEVMKKNMMFIKTCACHYNCPGDNDIFESLYYRKMYGDMA 172
```

RESULT 2
AAW12694
```
ID   AAW12694 standard; protein; 347 AA.
XX
AC   AAW12694;
XX
DT   25-MAR-2003  (revised)
DT   31-MAY-1997  (first entry)
XX
DE   Connective tissue growth factor.
XX
KW   Connective tissue growth factor; CTGF; bone; cartilage; vulnerary;
KW   wound healing; osteoporosis; osteoarthritis; osteochondrytis.
XX
OS   Mus sp.
XX
XX
PN   WO9638168-A1.
XX
PD   05-DEC-1996.
XX
PF   31-MAY-1995;  96WO-US008210.
XX
PR   02-JUN-1995;  95US-00459717.
PR   31-MAY-1996;  96WO-US008140.
XX
PA   (GROT/) GROTENDORST G R.
XX
PI   Grotendorst GR;
XX
DR   WPI; 1997-042658/04.
DR   N-PSDB; AAT59618.
XX
PT   Connective Tissue Growth Factor composition - for inducing bone, tissue
PT   and cartilage formation and wound healing.
XX
PS   Disclosure; Fig 1C1-3; 60pp; English.
XX
CC   Connective tissue growth factor (CTGF) (AAW12694) is a cysteine-rich
CC   mitogenic protein which is selectively induced in fibroblasts after
CC   activation with transforming growth factor beta (TGF-beta). Recombinant
CC   CTGF can be produced in prokaryotic or eukaryotic host cells utilising an
CC   isolated CTGF gene (AAT59618). Compsns. comprising CTGF, pref. in
CC   combination with TGF-beta, are used to induce bonding formation, e.g. to
CC   treat osteoporosis, osteoarthritis and osteochondrytis, to induce tissue
CC   and cartilage formation, and to induce wound healing. It can also be used
CC   in culture systems e.g. to expand stem cells or chondrocytes prior to re-
CC   implantation. CTGF is more stable to protease degradation than other
CC   growth factors used as prior art wound healing agents. (Updated on 25-MAR
CC   -2003 to correct PR field.)
```

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SQ   Sequence 347 AA;

Query Match             100.0%;  Score 956;  DB 2;  Length 347;
Best Local Similarity   100.0%;  Pred. No. 3.9e-85;
Matches 172;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Qy    1 ALAAYRLEDTFGPDPTMIRANCLVQTTEWSACSKTCGMGISTRVTNDNASCRLEKQSRLC 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  176 ALAAYRLEDTFGPDPTMIRANCLVQTTEWSACSKTCGMGISTRVTNDNASCRLEKQSRLC 235

Qy   61 MVRPCEADLEENIKKGKHKCIRTPKISKPIKFELSGCTSMKTYRAKFCGVCTDGRCCTPHR 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  236 MVRPCEADLEENIKKGKHKCIRTPKISKPIKFELSGCTSMKTYRAKFCGVCTDGRCCTPHR 295

Qy  121 TTTLPVEFKCPDGEVMKKNMMFIKTCACHYNCPGDNDIFESLYYRKMYGDMA 172
        |||||||||||||||||||||||||||||||||||||||||||||||||||
Db  296 TTTLPVEFKCPDGEVMKKNMMFIKTCACHYNCPGDNDIFESLYYRKMYGDMA 347
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RESULT 3
ABB09204
```
ID   ABB09204 standard; protein; 348 AA.
XX
AC   ABB09204;
XX
DT   08-JUL-2002  (first entry)
XX
DE   Human ctgf CNN family protein sequence SEQ ID NO:14.
XX
KW   Human; small CCN-like growth factor; SCGF; vulnerary; osteopathic;
KW   gene therapy; muscle wasting disease; osteoporosis; wound healing;
KW   tissue regeneration; angiogenesis.
XX
OS   Homo sapiens.
XX
PN   US2002049304-A1.
XX
PD   25-APR-2002.
XX
PF   14-MAY-2001;  2001US-00853625.
XX
PR   06-JUN-1995;  95US-00468847.
PR   01-APR-1998;  98US-00053587.
XX
PA   (HAST/) HASTINGS G A.
PA   (ADAM/) ADAMS M D.
XX
PI   Hastings GA, Adams MD;
XX
DR   WPI; 2002-382150/41.
XX
PT   Novel isolated polynucleotide sequence encoding a human small CCN-like
PT   growth factor, useful for treating muscle wasting disease, and
PT   osteoporosis.
XX
PS   Disclosure; Fig 2A-D; 33pp; English.
XX
CC   The present invention describes human small CCN-like growth factor
CC   (SCGF). SCGF has vulnerary and osteopathic activities, and can be used in
CC   gene therapy. The SCGF polypeptides and polynucleotides can be used for
CC   treating muscle wasting diseases, and osteoporosis, and to stimulate
CC   wound healing and tissue regeneration, to promote angiogenesis and to
CC   stimulate proliferation of vascular smooth muscle and endothelial cell
CC   production. The present sequence represents a CNN family protein which is
CC   given in comparison with the human SCGF in the exemplification of the
CC   present invention
XX
SQ   Sequence 348 AA;

Query Match             100.0%;  Score 956;  DB 5;  Length 348;
Best Local Similarity   100.0%;  Pred. No. 3.9e-85;
Matches 172;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;
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RESULT 4
AAR79964
ID   AAR79964 standard; protein; 349 AA.
XX
AC   AAR79964;
XX
DT   25-MAR-2003 (revised)
DT   12-JUN-1996 (first entry)
XX
DE   Connective tissue growth factor.
XX
KW   Connective tissue growth factor; CTGF; wound healing; vulnerary;
KW   cell proliferation; cancer; fibrosis; atherosclerosis; diagnosis therapy;
KW   mitogen.
XX
OS   Homo sapiens.
XX
FH   Key   Location/Qualifiers
FT   Modified-site 28
FT   /label= N-glycosylation_site
FT   Modified-site 225
FT   /label= N-glycosylation_site
XX
PN   US5408040-A.
XX
PD   18-APR-1995.
XX
PF   14-DEC-1993; 93US-0167628.
XX
PR   30-AUG-1991; 91US-00752427.
XX
PA   (UYSF-) UNIV SOUTH FLORIDA.
XX
PI   Bradham DM, Grotendorst GR;
XX
DR   WPI; 1995-161147/21.
DR   N-PSDB; AAT04226.
XX
PT   New connective tissue growth factor - used to develop prods. for wound
PT   healing and for diagnosis and therapy of cell proliferative disorders.
XX
PS   Claim 1; Col 19-20; 12pp; English.
XX
CC   Novel human connective tissue growth factor (CTGF) (AAR79964) is related
CC   immunologically and biologically to platelet-derived growth factor
CC   (PDGF), but is the product of a distinct gene. CTGF is mitogenic and also
CC   a chemotactic agent for cells. It is produced by endothelial and
CC   fibroblastic cells, and probably acts as a growth factor in wound
CC   healing. Recombinant CTGF can be obtd. by expression of cDNA clone
CC   DB60R32 (AAT04226) in transformed host cells. It is used to accelerate
CC   wound healing, and to raise antibodies useful in detecting disorders
CC   associated with overgrowth of cells, such as cancer, fibrotic diseases
CC   and atherosclerosis. (Updated on 25-MAR-2003 to correct PF field.)
XX
SQ   Sequence 349 AA;

Query Match   100.0%; Score 956; DB 2; Length 349;
Best Local Similarity 100.0%; Pred. No. 3.9e-85;
Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   1 ALAAYRLEDTFGPDPTMIRANCLVQTTEWSACSKTCGMGISTRVTNDNASCRLEKQSRLC 60
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 177 ALAAYRLEDTFGPDPTMIRANCLVQTTEWSACSKTCGMGISTRVTNDNASCRLEKQSRLC 236

Qy   61 MVRPCEADLEENIKKGKKCIRTPKISKPIKFELSGCTSMKTYRAKFCGVCTDGRCCTPHR 120
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 237 MVRPCEADLEENIKKGKKCIRTPKISKPIKFELSGCTSMKTYRAKFCGVCTDGRCCTPHR 296

Qy 121 TTTLPVEFKCPDGEVMKKNMMFIKTCACHYNCPGDNDIFESLLYRKMYGDMA 172
        |||||||||||||||||||||||||||||||||||||||||||||||||||
Db 297 TTTLPVEFKCPDGEVMKKNMMFIKTCACHYNCPGDNDIFESLLYRKMYGDMA 348

RESULT 5
AAW11302
ID   AAW11302 standard; protein; 349 AA.
XX
AC   AAW11302;
XX
DT   25-MAR-2003 (revised)
DT   18-MAR-1997 (first entry)
XX
DE   Connective tissue growth factor.
XX
KW   Connective tissue growth factor; CTGF; human; connective tissue cell;
KW   proliferative disease; platelet-derived growth factor; development;
KW   tissue growth; repair; umbilical vein endothelial cell; HUVE cell;
KW   antibody; wound healing; cancer; fibrotic disease; atherosclerosis;
KW   inhibitor; protease degradation; growth factor; therapy.
XX
OS   Homo sapiens.
XX
PN   US5585270-A.
XX
PD   17-DEC-1996.
XX
PF   10-FEB-1995; 95US-00386680.
XX
PR   30-AUG-1991; 91US-00752427.
PR   14-DEC-1993; 93US-0167628.
XX
PA   (UYSF-) UNIV SOUTH FLORIDA.
XX
PI   Grotendorst GR, Bradham DM;
XX
DR   WPI; 1997-051180/05.
DR   N-PSDB; AATS1234.
XX
PT   New nucleic acid encoding connective tissue growth factor - useful for
PT   accelerating wound healing, also for diagnosis and treatment of
PT   proliferative disease.
XX
PS   Claim 9; Col 15-18; 11pp; English.
XX
CC   This sequence represents the human connective tissue growth factor
CC   (CTGF). CTGF is related immunologically and biologically to platelet-
CC   derived growth factor (PDGF), but is encoded by an unrelated gene. CTGF
CC   is thought to play a significant role in the normal development, growth,
CC   and repair of human tissue, similarly to PDGF. The cDNA encoding this
CC   sequence was isolated by screening a cDNA library from human umbilical
CC   vein endothelial (HUVE) cells with anti-PDGF antibodies. CTGF can be used
CC   to accelerate wound healing. Also, elevated levels of CTGF may be
CC   diagnostic of proliferative diseases involving outgrowth of connective
CC   tissue cells, such as cancer, fibrotic disease and atherosclerosis. All
CC   of these diseases can be treated with reagents reactive with CTGF, such
CC   as antibodies (which can also serve as assay reagents). Antisense nucleic
CC   acids, and ribozymes could also be used to inhibit CTGF production. The
CC   advantage with using CTGF is that it is more stable, and less susceptible
CC   to protease degradation than PDGF, and other growth factors involved in
CC   wound healing. This is believed to be due to the high Cys content.
CC   (Updated on 25-MAR-2003 to correct PF field.)
XX
SQ   Sequence 349 AA;

Qy   1 ALAAYRLEDTFGPDPTMIRANCLVQTTEWSACSKTCGMGISTRVTNDNASCRLEKQSRLC 60
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 178 ALAAYRLEDTFGPDPTMIRANCLVQTTEWSACSKTCGMGISTRVTNDNASCRLEKQSRLC 237

Qy   61 MVRPCEADLEENIKKGKKCIRTPKISKPIKFELSGCTSMKTYRAKFCGVCTDGRCCTPHR 120
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 238 MVRPCEADLEENIKKGKKCIRTPKISKPIKFELSGCTSMKTYRAKFCGVCTDGRCCTPHR 297

Qy 121 TTTLPVEFKCPDGEVMKKNMMFIKTCACHYNCPGDNDIFESLLYRKMYGDMA 172
        |||||||||||||||||||||||||||||||||||||||||||||||||||
Db 298 TTTLPVEFKCPDGEVMKKNMMFIKTCACHYNCPGDNDIFESLLYRKMYGDMA 349

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Qy   Query Match             100.0%;   Score 956;  DB 2;  Length 349;
     Best Local Similarity   100.0%;   Pred. No. 3.9e-85;
     Matches  172;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy      1 ALAAYRLEDTFGPDPTMIRANCLVQTTEWSACSKTCGMGISTRVTNDNASCRLEKQSRLC 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    178 ALAAYRLEDTFGPDPTMIRANCLVQTTEWSACSKTCGMGISTRVTNDNASCRLEKQSRLC 237

Qy     61 MVRPCEADLEENIKKGKKCIRTPKISKPIKFELSGCTSMKTYRAKFCGVCTDGRCCTPHR 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    238 MVRPCEADLEENIKKGKKCIRTPKISKPIKFELSGCTSMKTYRAKFCGVCTDGRCCTPHR 297

Qy    121 TTTLPVEFKCPDGEVMKKNMMFIKTCACHYNCPGDNDIFESLYYRKMYGDMA 172
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db    298 TTTLPVEFKCPDGEVMKKNMMFIKTCACHYNCPGDNDIFESLYYRKMYGDMA 349


RESULT 6
AAW09089
ID   AAW09089 standard; protein; 349 AA.
XX
AC   AAW09089;
XX
DT   25-MAR-2003  (revised)
DT   26-APR-1997  (first entry)
XX
DE   Human connective tissue growth factor.
XX
KW   Connective tissue growth factor; CTGF; mitogen; cell proliferation;
KW   wound healing; cancer; tumour; fibrosis; glaucoma; atherosclerosis;
KW   scleroderma; arthritis, cirrhosis; scar; diagnosis; therapy.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FH
FT   Modified-site   28
FT                   /label= Glycosylation
FT                   /note= "potential N-glycosylation site"
FT   Modified-site   225
FT                   /label= Glycosylation
FT                   /note= "potential N-glycosylation site"
XX
PN   WO9638172-A1.
XX
PD   05-DEC-1996.
XX
PF   31-MAY-1996;  96WO-US008140.
XX
PR   02-JUN-1995;  95US-00459717.
PR   31-MAY-1996;  96WO-US008140.
XX
PA   (UYSF-)  UNIV SOUTH FLORIDA.
XX
PI   Grotendorst GR;  Bradham DM;
XX
DR   WPI; 1997-042659/04.
DR   N-PSDB; AAT45360, AAT58534.
XX
PT   Connective tissue growth factor coding sequence and protein - used in the
PT   treatment of proliferative disorders and to accelerate wound healing.
XX
PS   Claim 19;  Page 50-52;  76pp;  English.
XX
CC   Novel human connective tissue growth factor (CTGF) (AAW09089) is a PDGF-
CC   unrelated protein that may play a significant role in the normal
CC   development, growth and repair of human tissue and probably functions as
CC   a growth factor in wound healing. CTGF may be involved in diseases in
CC   which there is an overgrowth of connective tissue cells, such as cancer,
CC   tumour formation and growth, fibrotic diseases (e.g. pulmonary fibrosis,
CC   kidney fibrosis, glaucoma) and atherosclerosis. Recombinant CTGF can be
CC   produced in transformed host cells utilizing a cDNA clone isolated from a
CC   HUVEC library. It can be used to accelerate wound healing. CTGF
CC   inhibitors can be used to treat atherosclerosis and fibrotic diseases
CC   such as scleroderma, arthritis, liver cirrhosis, and scarring. (Updated
CC   on 25-MAR-2003 to correct PR field.)
XX
SQ   Sequence 349 AA;


Qy   Query Match             100.0%;   Score 956;  DB 2;  Length 349;
     Best Local Similarity   100.0%;   Pred. No. 3.9e-85;
     Matches  172;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy      1 ALAAYRLEDTFGPDPTMIRANCLVQTTEWSACSKTCGMGISTRVTNDNASCRLEKQSRLC 60
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Qy     61 MVRPCEADLEENIKKGKKCIRTPKISKPIKFELSGCTSMKTYRAKFCGVCTDGRCCTPHR 120
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Qy    121 TTTLPVEFKCPDGEVMKKNMMFIKTCACHYNCPGDNDIFESLYYRKMYGDMA 172
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db    298 TTTLPVEFKCPDGEVMKKNMMFIKTCACHYNCPGDNDIFESLYYRKMYGDMA 349


RESULT 7
AAW62084
ID   AAW62084 standard; protein; 349 AA.
XX
AC   AAW62084;
XX
DT   15-SEP-1998  (first entry)
XX
DE   Human connective tissue growth factor.
XX
KW   Human; connective tissue growth factor; CTGF; PDGF; diagnosis; cancer;
KW   platelet derived growth factor; ameliorating cell proliferative disorder;
KW   atherosclerosis; fibrotic disease.
XX
OS   Homo sapiens.
XX
PN   US5783187-A.
XX
PD   21-JUL-1998.
XX
PF   11-SEP-1996;  96US-00712302.
XX
PR   30-AUG-1991;  91US-00752427.
PR   14-DEC-1993;  93US-00167628.
XX
PA   (UYSF-)  UNIV SOUTH FLORIDA.
XX
PI   Bradham DM,  Grotendorst GR;
XX
DR   WPI; 1998-426958/36.
DR   N-PSDB; AAV38085.
XX
PT   Ameliorating cell proliferative disorder associated with connective
PT   tissue growth factor - comprises the administration of an antibody which
PT   binds to connective tissue growth factor and not to platelet-derived
PT   growth factor.
XX
PS   Example 6;  Col 17-20;  11pp;  English.
XX
CC   A method has been developed for ameliorating a cell proliferative
CC   disorder associated with connective tissue growth factor (CTGF). The
CC   method comprises the administration of an antibody or its fragment that
CC   binds to CTGF and not to platelet-derived growth factor (PDGF), to the
CC   site of the disorder. CTGF is related immunologically and biologically to
CC   PDGF. The present sequence represents CTGF. The method is used to treat
CC   conditions involving the overgrowth of connective tissue cells such as
CC   cancer, atherosclerosis and other fibrotic diseases
XX
SQ   Sequence 349 AA;
```

```
Qy  Query Match
    Best Local Similarity  100.0%;   Score 956;  DB 2;  Length 349;
                  100.0%;            Pred. No. 3.9e-85;
    Matches 172;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

Qy    1 ALAAYRLEDTFGPDPTMIRANCLVQTTEWSACSKTCGMGISTRVTNDNASCRLEKQSRLC 60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  178 ALAAYRLEDTFGPDPTMIRANCLVQTTEWSACSKTCGMGISTRVTNDNASCRLEKQSRLC 237

Qy   61 MVRPCEADLEENIKKGKKCIRTPKISKPIKFELSGCTSMKTYRAKFCGVCTDGRCCTPHR 120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  238 MVRPCEADLEENIKKGKKCIRTPKISKPIKFELSGCTSMKTYRAKFCGVCTDGRCCTPHR 297

Qy  121 TTTLPVEFKCPDGEVMKKNMMFIKTCACHYNCPGDNDIFESLYYRKMYGDMA 172
         |||||||||||||||||||||||||||||||||||||||||||||||||||
Db  298 TTTLPVEFKCPDGEVMKKNMMFIKTCACHYNCPGDNDIFESLYYRKMYGDMA 349
```

```
RESULT 8
AAW81425;
ID   AAW81425 standard; protein; 349 AA.
XX
AC   AAW81425;
XX
DT   25-JAN-1999 (first entry)
XX
DE   Connective tissue growth factor (CTGF).
XX
KW   CTGF; connective tissue growth factor; bone formation; tissue; arthritis;
KW   wound healing; cartilage formation; osteoporosis; osteoarthritis; burn;
KW   osteochondrytis; skeletal disorder; hypertrophic scar; protease; PDGF;
KW   degradation; vascular hypertrophy; platelet derived growth factor.
XX
OS   Homo sapiens.
XX
FH   Key               Location/Qualifiers
FT   Peptide           1..21
FT                     /note= "signal peptide"
FT   Protein           22..349
FT                     /note= "mature protein"
XX
PN   US5837258-A.
XX
PD   17-NOV-1998.
XX
PF   31-MAY-1996;  96US-00656393.
XX
PR   30-AUG-1991;  91US-00752427.
PR   14-DEC-1993;  93US-00167628.
PR   10-FEB-1995;  95US-00386680.
PR   02-JUN-1995;  95US-00459717.
XX
PA   (UYSF-) UNIV SOUTH FLORIDA.
PA   (UYMI-) UNIV MIAMI.
XX
PI   Grotendorst GR;
XX
DR   WPI; 1999-023382/02.
DR   N-PSDB; AAV65380.
XX
PT   Use of connective tissue growth factor - for inducing bone, tissue or
PT   cartilage formation in a patient or for inducing wound healing.
XX
PS   Disclosure; Fig 1C; 30pp; English.
XX
CC   This represents the amino acid sequence of connective tissue growth
CC   factor (CTGF). This can be used in the method of the invention for
CC   inducing bone or tissue formation that comprises administration to a
CC   patient, a composition comprising CTGF and a carrier. CTGF can also be
CC   used in a method for inducing wound healing. The methods can be used for
CC   inducing bone, tissue or cartilage formation in disorders such as
CC   osteoporosis, osteoarthritis or osteochondrytis, arthritis, skeletal
CC   disorders, hypertrophic scar, burns, vascular hypertrophy, or in wound
CC   healing. The CTGF and functional fragments are more stable and less
CC   susceptible to protease degradation than platelet derived growth factor
CC   (PDGF) and other growth factors known to be involved in wound healing
XX
SQ   Sequence 349 AA;
```

```
Qy  Query Match
    Best Local Similarity  100.0%;   Score 956;  DB 2;  Length 349;
                  100.0%;            Pred. No. 3.9e-85;
    Matches 172;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

Qy    1 ALAAYRLEDTFGPDPTMIRANCLVQTTEWSACSKTCGMGISTRVTNDNASCRLEKQSRLC 60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  178 ALAAYRLEDTFGPDPTMIRANCLVQTTEWSACSKTCGMGISTRVTNDNASCRLEKQSRLC 237

Qy   61 MVRPCEADLEENIKKGKKCIRTPKISKPIKFELSGCTSMKTYRAKFCGVCTDGRCCTPHR 120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  238 MVRPCEADLEENIKKGKKCIRTPKISKPIKFELSGCTSMKTYRAKFCGVCTDGRCCTPHR 297

Qy  121 TTTLPVEFKCPDGEVMKKNMMFIKTCACHYNCPGDNDIFESLYYRKMYGDMA 172
         |||||||||||||||||||||||||||||||||||||||||||||||||||
Db  298 TTTLPVEFKCPDGEVMKKNMMFIKTCACHYNCPGDNDIFESLYYRKMYGDMA 349
```

```
RESULT 9
AAY18361
ID   AAY18361 standard; protein; 349 AA.
XX
AC   AAY18361;
XX
DT   20-AUG-1999 (first entry)
XX
DE   Human connective tissue growth factor.
XX
KW   CTGF; connective tissue growth factor; human; fibrotic disease;
KW   cell proliferative disorder; atherosclerosis; diagnosis.
XX
OS   Homo sapiens.
XX
PN   US5916756-A.
XX
PD   29-JUN-1999.
XX
PF   20-JUN-1997;  97US-00880031.
XX
PR   14-DEC-1993;  93US-00167628.
PR   10-FEB-1995;  95US-00386680.
PR   11-SEP-1996;  96US-00712302.
XX
PA   (UYSF-) UNIV SOUTH FLORIDA.
XX
PI   Bradham DM, Grotendorst GR;
XX
DR   WPI; 1999-384720/32.
DR   N-PSDB; AAX61317.
XX
PT   Detecting cell proliferative disorders such as fibrotic disease and
PT   atherosclerosis.
XX
PS   Disclosure; Col 15-18; 11pp; English.
XX
CC   This sequence is the human connective tissue growth factor (CTGF). The
CC   invention relates to a method of detecting a cell proliferative disorder
CC   comprising comparing the level of CTGF in a sample against a control,
CC   where an increase is indicative of a cell proliferative disorder
CC   (fibrotic disease or atherosclerosis). The method is used to detect cell
CC   proliferative disorders such as fibrotic disease and atherosclerosis.
XX
SQ   Sequence 349 AA;
```

```
Qy  Query Match
    Best Local Similarity  100.0%;   Score 956;  DB 2;  Length 349;
                  100.0%;            Pred. No. 3.9e-85;
    Matches 172;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

Qy    1 ALAAYRLEDTFGPDPTMIRANCLVQTTEWSACSKTCGMGISTRVTNDNASCRLEKQSRLC 60
```

```
Db   178 ALAAYRLEDTFGPDPTMIRANCLVQTTEWSACSKTCGMGISTRVTNDNASCRLEKQSRLC 237
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    61 MVRPCEADLEENIKKGKKCIRTPKISKPIKFELSGCTSMKTYRAKFCGVCTDGRCCTPHR 120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   238 MVRPCEADLEENIKKGKKCIRTPKISKPIKFELSGCTSMKTYRAKFCGVCTDGRCCTPHR 297

Qy   121 TTTLPVEFKCPDGEVMKKNMMFIKTCACHYNCPGDNDIFESLYYRKMYGDMA 172
         |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   298 TTTLPVEFKCPDGEVMKKNMMFIKTCACHYNCPGDNDIFESLYYRKMYGDMA 349
```

```
RESULT 10
AAY92939
ID   AAY92939 standard; protein; 349 AA.
XX
AC   AAY92939;
XX
DT   08-NOV-2000  (first entry)
XX
DE   Human connective tissue growth factor protein.
XX
KW   Dermatological; antiarthritic; antiarteriosclerotic; antidiabetic;
KW   nephrotropic; ophthalmological; hypotensive; cardiant; tranquilizer;
KW   vulnerary; antiinflammatory; human; connective tissue growth factor;
KW   CTGF; extracellular matrix synthesis; collagen synthesis; antibody;
KW   myofibroblast differentiation; antisense; fibroproliferative disease;
KW   fibrosis; trauma; cancer; inflammation; diabetes; keloid.
XX
OS   Homo sapiens.
XX
PN   WO200035936-A1.
XX
PD   22-JUN-2000.
XX
PF   14-DEC-1999;   99WO-US029652.
XX
PR   14-DEC-1998;   98US-0112240P.
PR   14-DEC-1998;   98US-0112241P.
XX
PA   (UYMI-) UNIV MIAMI.
XX
PI   Grotendorst GR;
XX
DR   WPI; 2000-431565/37.
DR   N-PSDB; AAA11278.
XX
PT   Fragment of connective tissue growth factor, useful for treating
PT   fibroproliferative diseases or disorders, including kidney fibrosis,
PT   scleroderma, arthritis, hypertropic scarring, atherosclerosis, diabetic
PT   nephropathy and retinopathy.
XX
PS   Claim 2, 3; Fig 3A-B; 74pp; English.
XX
CC   This sequence represents a human connective tissue growth factor (CTGF)
CC   polypeptide having the ability to induce extracellular matrix synthesis,
CC   collagen synthesis and/or myofibroblast differentiation. The invention
CC   relates to fragments of CTGF, especially those encoded by exons 2 and/or
CC   3, which contain the inductive activity. The protein and/or fragments can
CC   be used to raise antibodies and the coding sequence can be used to
CC   generate antisense oligonucleotides. The antibody or antisense sequence
CC   against the CTGF sequence can be used in a method to treat a CTGF-
CC   associated disease or disorder such as a fibroproliferative disease or
CC   disorder, especially selected from kidney fibrosis, hypertropic scarring,
CC   pulmonary fibrosis, liver fibrosis, arthritis, scleroderma,
CC   atherosclerosis, diabetic nephropathy and retinopathy, hypertension,
CC   kidney disorders, angiogenesis-related disorders, skin fibrotic
CC   disorders, and cardiovascular disorders. The disease or disorder can also
CC   be selected from acute or repetitive traumas (including surgery or
CC   radiation therapy, and fibrosis of organs), diseases caused by vascular
CC   endothelial cell proliferation or migration (including cancers),
CC   inflammatory bowel disease, Crohn's disease, joint inflammation,
CC   interstitial disease, dermatological diseases, diabetes, and keloids
```

```
XX
SQ   Sequence 349 AA;
XX
Query Match     100.0%;  Score 956;  DB 3;  Length 349;
Best Local Similarity   100.0%;  Pred. No. 3.9e-85;
Matches 172;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy     1 ALAAYRLEDTFGPDPTMIRANCLVQTTEWSACSKTCGMGISTRVTNDNASCRLEKQSRLC 60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   178 ALAAYRLEDTFGPDPTMIRANCLVQTTEWSACSKTCGMGISTRVTNDNASCRLEKQSRLC 237

Qy    61 MVRPCEADLEENIKKGKKCIRTPKISKPIKFELSGCTSMKTYRAKFCGVCTDGRCCTPHR 120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   238 MVRPCEADLEENIKKGKKCIRTPKISKPIKFELSGCTSMKTYRAKFCGVCTDGRCCTPHR 297

Qy   121 TTTLPVEFKCPDGEVMKKNMMFIKTCACHYNCPGDNDIFESLYYRKMYGDMA 172
         |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   298 TTTLPVEFKCPDGEVMKKNMMFIKTCACHYNCPGDNDIFESLYYRKMYGDMA 349
```

```
RESULT 11
AAY92940
ID   AAY92940 standard; protein; 349 AA.
XX
AC   AAY92940;
XX
DT   08-NOV-2000  (first entry)
XX
DE   Human connective tissue growth factor protein.
XX
KW   Human; connective tissue growth factor; CTGF; mitogen; antibody; liver;
KW   fibroproliferative disease; scleroderma; fibrosis; kidney; arthritis;
KW   hypertropic scarring; atherosclerosis; diabetic nephropathy; retinopathy;
KW   hypertension; cardiovascular disorder; wound healing; bone repair.
XX
OS   Homo sapiens.
XX
PN   WO200035939-A2.
XX
PD   22-JUN-2000.
XX
PF   14-DEC-1999;   99WO-US029654.
XX
PR   14-DEC-1998;   98US-0112240P.
PR   14-DEC-1998;   98US-0112241P.
XX
PA   (UYMI-) UNIV MIAMI.
PA   (FIBR-) FIBROGEN INC.
XX
PI   Grotendorst GR, Neff TB;
XX
DR   WPI; 2000-431568/37.
DR   N-PSDB; AAA11280.
XX
PT   New fragment of connective tissue growth factor (CTGF) polypeptide having
PT   mitogenic activity, useful in wound healing, bone and tissue repair.
XX
PS   Claim 2, 3; Fig 2A-B; 71pp; English.
XX
CC   This sequence represents a human connective tissue growth factor (CTGF)
CC   polypeptide which has mitogenic activity. The protein can be used to
CC   raise antibodies which specifically bind to CTFG and are used to treat a
CC   CTGF-associated disease or disorder, e.g. a fibroproliferative
CC   disease/disorder such as kidney fibrosis, scleroderma, pulmonary
CC   fibrosis, liver fibrosis, arthritis, hypertropic scarring,
CC   atherosclerosis, diabetic nephropathy and retinopathy, hypertension,
CC   kidney disorders, angiogenesis-related disorders, skin fibrotic
CC   disorders, and cardiovascular disorders. The protein is also useful in
CC   wound healing, bone and tissue repair

XX
SQ   Sequence 349 AA;

Query Match     100.0%;  Score 956;  DB 3;  Length 349;
```

Beet Local Similarity 100.0%; 0; Pred. No. 3.9e-85; Mismatches 0; Indels 0; Gaps 0;
Matches 172; Conservative

```
Qy   1 ALAAYRLEDTFGPDPTMIRANCLVQTTEWSACSKTCGMGISTRVTNDNASCRLEKQSRLC  60
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 178 ALAAYRLEDTFGPDPTMIRANCLVQTTEWSACSKTCGMGISTRVTNDNASCRLEKQSRLC 237

Qy  61 MVRPCEADLEENIKKGKKCIRTPKISKPIKFELSGCTSMKTYRAKFCGVCTDGRCCTPHR 120
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 238 MVRPCEADLEENIKKGKKCIRTPKISKPIKFELSGCTSMKTYRAKFCGVCTDGRCCTPHR 297

Qy 121 TTTLPVEFKCPDGEVMKKNMMFIKTCACHYNCPGDNDIFESLYYRKMYGDMA 172
        |||||||||||||||||||||||||||||||||||||||||||||||||||
Db 298 TTTLPVEFKCPDGEVMKKNMMFIKTCACHYNCPGDNDIFESLYYRKMYGDMA 349
```

RESULT 12
ID   AAY44755
     AAY44755 standard; protein; 349 AA.
XX
AC   AAY44755;
XX
DT   04-MAY-2000 (first entry)
XX
DE   Human connective tissue growth factor.
XX
KW   Connective tissue growth factor; CCN growth regulator; angiogenesis;
KW   antiangiogenic; basic fibroblast growth factor; bFGF; neovascular;
KW   endothelial cell proliferation; retinal; haemangioma; leukaemia;
KW   metastasis; psoriasis; tumour; glaucoma; diabetic retinopathy; arthritis;
KW   endometriosis; Insulin-like growth factor-binding domain; IGF;
KW   von Willebrand factor type C repeat; Thrombospondin type 1 domain;
KW   C-terminal cysteine knot profile; CTCK-2; human.
XX
OS   Homo sapiens.
XX
PN   WO20005356-A1.
XX
PD   03-FEB-2000.
XX
PF   11-JUN-1999;   99WO-US013338.
PF   21-JUL-1998;   98US-00119804.
XX
PR
PA   (CHIL-) CHILDRENS MEDICAL CENT.
XX
PI   Folkman J, Lin J;
XX
DR   WPI; 2000-182688/16.
XX
PT   New anti-angiogenic protein containing an IGF binding, Willebrand factor
PT   type C, thrombospondin type 1 and cysteine knot domains is useful for
PT   inhibiting atopic angiogenesis e.g. in solid tumors.
XX
PS   Claim 6; Page 26-27; 30pp; English.
XX
CC   The present sequence is human connective tissue growth factor, which is a
CC   member of CCN growth regulator family. It has antiangiogenic activity and
CC   is a potent inhibitor of basic fibroblast growth factor (bFGF)-stimulated
CC   bovine endothelial cell proliferation. It contains Insulin-like growth
CC   factor (IGF)-binding domain, von Willebrand factor type C repeat,
CC   Thrombospondin type 1 domain and C-terminal cysteine knot profile (CTCK)-
CC   2 domain. It can be used to treat conditions associated with abnormal
CC   angiogenesis or neovascularisation like, retinal neovascularisation,
CC   tumour growth, haemangioma, solid tumours, leukaemia, metastasis,
CC   psoriasis, neovascular glaucoma, diabetic retinopathy, arthritis,
CC   endometriosis and premature retinopathy.

SQ   Sequence 349 AA;

Query Match   100.0%;
Score 956; DB 3; Length 349;
Best Local Similarity   100.0%;   Pred. No. 3.9e-85;
Matches 172; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

```
Qy   1 ALAAYRLEDTFGPDPTMIRANCLVQTTEWSACSKTCGMGISTRVTNDNASCRLEKQSRLC  60
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 178 ALAAYRLEDTFGPDPTMIRANCLVQTTEWSACSKTCGMGISTRVTNDNASCRLEKQSRLC 237

Qy  61 MVRPCEADLEENIKKGKKCIRTPKISKPIKFELSGCTSMKTYRAKFCGVCTDGRCCTPHR 120
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 238 MVRPCEADLEENIKKGKKCIRTPKISKPIKFELSGCTSMKTYRAKFCGVCTDGRCCTPHR 297

Qy 121 TTTLPVEFKCPDGEVMKKNMMFIKTCACHYNCPGDNDIFESLYYRKMYGDMA 172
        |||||||||||||||||||||||||||||||||||||||||||||||||||
Db 298 TTTLPVEFKCPDGEVMKKNMMFIKTCACHYNCPGDNDIFESLYYRKMYGDMA 349
```

RESULT 13
ID   AAB84598
     AAB84598 standard; protein; 349 AA.
XX
AC   AAB84598;
XX
DT   05-SEP-2001 (first entry)
XX
DE   Amino acid sequence of connective tissue derived growth factor.
XX
KW   Growth factor; protein inhibitor; protease; damaged tissue;
KW   platelet-derived growth factor; PDGF; fibroblast growth factor; FGF;
KW   connective tissue derived growth factor; CTGF; chrysalin; VEGF;
KW   keratinocyte-derived growth factor; KGF; epidermal growth factor; EGF;
KW   transforming growth factor-beta; TGF-beta; matrix metalloproteinase; MMP;
KW   granulocyte macrophage colony stimulating factor; GM-CSF; uPA;
KW   vascular endothelial growth factor; urokinase plasminogen activator;
KW   dermal ulcer; wound.
XX
OS   Homo sapiens.
XX
PN   WO200149309-A2.
XX
PD   12-JUL-2001.
XX
PF   21-DEC-2000;   2000WO-IB001935.
XX
PR   29-DEC-1999;   99GB-0030768.
XX
PA   (PFIZ) PFIZER LTD.
PA   (PFIZ) PFIZER INC.
XX
PI   Davies MJ, Huggins JP, McIntosh FS, Occleston NL;
XX
DR   WPI; 2001-418351/44.
DR   N-PSDB; AAH28213.
XX
PT   Composition for the treatment of damaged tissue i.e. chronic wounds and
PT   dermal ulcers comprises an inhibitor agent i.e. a protease and a growth
PT   factor.
XX
PS   Disclosure; Page 543; 572pp; English.
XX
CC   The specification describes a pharmaceutical composition, comprising a
CC   growth factor, an inhibitor agent, i.e. a protease. The inhibitor agent
CC   inhibits the action of at least one specific adverse protein, i.e. a
CC   protease, that is upregulated in a damaged tissue such as a wound
CC   environment. Growth factors which are included in the composition of the
CC   invention are platelet-derived growth factor (PDGF), fibroblast growth
CC   factor (FGF), connective tissue derived growth factor (CTGF),
CC   keratinocyte-derived growth factor (KGF), transforming growth factor-beta
CC   (TGF-beta), granulocyte macrophage colony stimulating factor (GM-CSF),
CC   epidermal growth factor (EGF), vascular endothelial growth factor (VEGF)
CC   and chrysalin. Inhibitors which are included in the composition of the
CC   invention include inhibitors of urokinase-type plasminogen activator
CC   (uPA) and matrix metalloproteinase (MMP). The composition is useful for
CC   the treatment of chronic damaged tissue, i.e. wounds and dermal ulcers.
CC   The present sequence represents a human CTGF, and is used to produce the
CC   composition of the invention

```
XX
SQ   Sequence 349 AA;

Qy   Best Local Similarity   100.0%;   Score 956;  DB 4;   Length 349;
     Matches 172;   Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;

Qy     1 ALAAYRLEDTFGPDPTMIRANCLVQTTEWSACSKTCGMGISTRVTNDNASCRLEKQSRLC 60
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   178 ALAAYRLEDTFGPDPTMIRANCLVQTTEWSACSKTCGMGISTRVTNDNASCRLEKQSRLC 237
```

RESULT 14
AAB90791
ID   AAB90791 standard; protein; 349 AA.
XX
AC   AAB90791;
XX
DT   15-JUN-2001 (first entry)
XX
DE   Human shear stress-response protein SEQ ID NO: 82.
XX
KW   Human; shear stress-response protein; vascular disease; arteriosclerosis.
XX
OS   Homo sapiens.
XX
PN   WO200125427-A1.
XX
PD   12-APR-2001.
XX
PF   02-OCT-2000; 2000WO-JP006840.
XX
PR   01-OCT-1999; 99JP-00280976.
XX
PA   (KYOW) KYOWA HAKKO KOGYO KK.
PI   (NOIJ/) NOJIMA H.
PI   Nojima H, Yoshigue H, Obayashi M, Ota T, Kawabata A, Sakurada K;
PI   Kuga T, Sekine S, Nakamura Y, Sugano S;
XX
DR   WPI; 2001-266308/27.
DR   N-PSDB; AAH02914.
XX
PT   DNA sequences, proteins encoded by them and antibodies against them
PT   useful in diagnosis and treatment of vascular disease caused by
PT   arteriosclerosis.
XX
PS   Claim 60; Page 460-462; 678pp; Japanese.
XX
CC   The present invention provides the protein and coding sequences of a
CC   number of human shear stress response proteins. These are useful in the
CC   diagnosis, treatment and screening of vascular diseases caused by
CC   arteriosclerosis, including heart failure, post-PTCA restenosis and
CC   hypertension
XX
SQ   Sequence 349 AA;

Qy   Best Local Similarity   100.0%;   Score 956; DB 4;   Length 349;
     Matches 172;   Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;

Qy   1 ALAAYRLEDTFGPDPTMIRANCLVQTTEWSACSKTCGMGISTRVTNDNASCRLEKQSRLC 60
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   178 ALAAYRLEDTFGPDPTMIRANCLVQTTEWSACSKTCGMGISTRVTNDNASCRLEKQSRLC 237

Qy   61 MVRPCEADLEENIKKGKKCIRTPKISKPIKFELSGCTSMKTYRAKFCGVCTDGRCCTPHR 120
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   238 MVRPCEADLEENIKKGKKCIRTPKISKPIKFELSGCTSMKTYRAKFCGVCTDGRCCTPHR 297

Qy   121 TTTLPVEFKCPDGEVMKKNMMPIKTCACHYNCPGDNDIFESLYYRKMYGDMA 172
         |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   298 TTTLPVEFKCPDGEVMKKNMMPIKTCACHYNCPGDNDIFESLYYRKMYGDMA 349
```

RESULT 15
AAB60664
ID   AAB60664 standard; protein; 349 AA.
XX
AC   AAB60664;
XX
DT   22-MAY-2001 (first entry)
XX
DE   Human connective tissue growth factor (CTGF).
XX
KW   Human; CTGF; connective tissue growth factor; recombinant production;
KW   mitogenic; chemotactic; tissue development; growth; repair;
KW   wound healing; vulnerary; diagnostic agent;
KW   cellular proliferation disorder.
XX
OS   Homo sapiens.
XX
PN   US6190884-B1.
XX
PD   20-FEB-2001.
XX
PF   18-MAY-1998; 98US-00080715.
XX
PR   30-AUG-1991; 91US-00754427.
PR   14-DEC-1993; 93US-00167628.
PR   10-FEB-1995; 95US-00386680.
PR   11-SEP-1996; 96US-00712302.
XX
PA   (UYSF-) UNIV SOUTH FLORIDA.
PI   Grotendorst GR, Bradham DM;
XX
DR   WPI; 2001-210379/21.
DR   N-PSDB; AAF59954.
XX
PS   Claim 1; Col 17-20; 11pp; English.
XX
CC   The invention relates to a method for the recombinant production of human
CC   connective tissue growth factor (CTGF; AAB60664), involving transforming
CC   a prokaryotic or eukaryotic host cell with an expression construct
CC   comprising the CTGF cDNA sequence (AAF59954) or a fragment thereof, and
CC   culturing the host cell under conditions suitable for the expression of
CC   CTGF. CTGF is a mitogen and chemotactic agent for connective tissue cells
CC   and plays a significant role in normal development, growth and repair of
CC   connective tissues. It is useful as a therapeutic for accelerating wound
CC   healing and promoting normal healing mechanisms and may therefore be used
CC   in the treatment of, e.g., burns. CTGF is also useful as a diagnostic
CC   reagent for diagnosing pathological states in a patient suspected of
CC   having a disease characterised by a disorder of cellular proliferation.
CC   The present sequence represents human CTGF
XX
SQ   Sequence 349 AA;

Qy   Best Local Similarity   100.0%;   Score 956;  DB 4;   Length 349;
     Matches 172;   Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;

Qy     1 ALAAYRLEDTFGPDPTMIRANCLVQTTEWSACSKTCGMGISTRVTNDNASCRLEKQSRLC 60
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   178 ALAAYRLEDTFGPDPTMIRANCLVQTTEWSACSKTCGMGISTRVTNDNASCRLEKQSRLC 237
```

```
Qy   61 MVRPCEADLEENIKKGKKCCIRTPKISKPIKFELSGCTSMKTYRAKFCGVCTDGRCCTPHR 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  238 MVRPCEADLEENIKKGKKCCIRTPKISKPIKFELSGCTSMKTYRAKFCGVCTDGRCCTPHR 297

Qy  121 TTTLPVEFKCPDGGEVMKKNMMFIKTCACHYNCPGDNDIFESLYYRKMYGDMA 172
        |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  298 TTTLPVEFKCPDGGEVMKKNMMFIKTCACHYNCPGDNDIFESLYYRKMYGDMA 349
```

Search completed: January 9, 2006, 11:16:16
Job time : 136 secs

This Page Blank (uspto)

```
OM protein - protein search, using sw model

                Copyright (c) 1993 - 2006 Compugen Ltd.
                GenCore version 5.1.6

Run on:         January 9, 2006, 11:11:27 ; Search time 40 Seconds
                                            (without alignments)
                                            413.732 Million cell updates/sec

Title:          US-09-461-646-4
Perfect score:  956
Sequence:       1 ALAAYRLEDTFGPDPTMIRA..........PGDNDIFESLYYRKMYGDMA 172

Scoring table:  BLOSUM62
                Gapop 10.0 , Gapext 0.5

Searched:       283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters:     283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :      PIR_80:*
                1: pir1:*
                2: pir2:*
                3: pir3:*
                4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

                         SUMMARIES

Result                     Query
No.     Score    Match     Length  DB  ID       Description
----    -----    -----     ------  --  --       -----------
  1     956      100.0     349     2   A40551   connective tissue
  2     934       97.7     348     2   A40578   beta IG-M2 protein
  3     546.5     57.2     357     2   S20078   NOV protein - chic
  4     519       54.3     357     2   I38069   gene novH protein
  5     487.5     51.0     379     2   A35669   gene CYR61 protein
  6     479.5     50.2     375     2   A41428   CEF-10 protein pre
  7     116       12.1     2165    2   T21371   hypothetical prote
  8     107       11.2     1444    2   T18856   angiogenesis inhib
  9     102.5     10.7     2098    2   T18397   protein CTRP - mal
 10     101.5     10.6     807     2   A38152   F-spondin - rat
 11      99       10.4     712     2   A45638   immunodominant mic
 12      99       10.4     803     2   A47723   F-spondin precurso
 13      97       10.1     4753    2   A47437   LDL-receptor-relat
 14      96.5     10.1     654     2   T29247   hypothetical prote
 15      96.5     10.1     898     2   T14764   hypothetical prote
 16      92        9.6     1205    2   T18517   procollagen N-endo
 17      92        9.6     1274    2   T42017   cysteine rich prot
 18      91        9.5     1059    2   T22545   hypothetical prote
 19      90.5      9.5     651     2   T19477   hypothetical prote
 20      90.5      9.5     1042    2   A57534   mucin SAC (clone L
 21      90.5      9.5     1372    2   T25933   hypothetical prote
 22      90.5      9.5     4006    2   T09070   probable tenascin
 23      89.5      9.4     388     2   A39756   circumsporozoite p
 24      89.5      9.4     1178    2   A39804   thrombospondin pre
 25      89        9.3     1558    2   C89114   protein C37C3.6a [
 26      89        9.3     2167    2   T34395   hypothetical prote
 27      88.5      9.3     104     2   S50911   metallothionein-2
 28      88        9.2     1025    2   T42626   secreted leucine-r
 29      88        9.2     2910    2   T42214   otogelin - mouse
 30      87.5      9.2     412     1   OZZQAF   circumsporozoite p
 31      87.5      9.2     424     2   A54533   circumsporozoite p
 32      87.5      9.2     442     2   A54529   circumsporozoite p
 33      87.5      9.2     957     2   T15976   hypothetical prote
 34      87        9.1     152     2   I47109   high-sulfur wool m
 35      87        9.1     732     2   S47073   finger protein H2F
 36      87        9.1     837     2   A42112   mucin-like peptide
 37      87        9.1     1170    2   TSHUP1   thrombospondin 1 p
 38      86        9.0     951     2   JC6164   circumsporozoite p
 39      86        9.0     1170    2   T00260   thrombospondin 1 p
 40      86        9.0     1170    2   A40558   thrombospondin 1 p
 41      85.5      8.9     724     2   A48569   antigen Em100 - Ei
 42      85        8.9     111     2   T34565   hypothetical prote
 43      85        8.9     152     2   KRSHHC   keratin high-sulfu
 44      85        8.9     152     2   I47112   high-sulfur wool m
 45      85        8.9     182     2   I47105   high-sulfur wool m
```

ALIGNMENTS

```
RESULT 1
A40551
connective tissue growth factor - human
C;Species: Homo sapiens (man)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 31-Dec-2004
C;Accession: A40551; S44205
R;Bradham, D.M.; Igarashi, A.; Potter, R.L.; Grotendorst, G.R.
J. Cell Biol. 114, 1285-1294, 1991
A;Title: Connective tissue growth factor: a cysteine-rich mitogen secreted by human vas
A;Reference number: A40551; MUID:91373462; PMID:1654338
A;Accession: A40551
A;Molecule type: mRNA
A;Residues: 1-349 <BRA>
A;Cross-references: UNIPROT:P29279; UNIPARC:UPI000003FD13; GB:M92934; GB:M36965; GB:S56.
R;Oemar, B.S.; Werner, A.; Yang, Z.; Garnier, J.M.; Gentz, R.; Luescher, T.F.
submitted to the EMBL Data Library, April 1994
A;Description: Differential cloning and expression of human connective tissue growth fa
A;Reference number: S44205
A;Accession: S44205
A;Status: Preliminary
A;Molecule type: mRNA
A;Residues: 1-349 <OEM>
A;Cross-references: UNIPARC:UPI000003FD13; EMBL:X78947; NID:g474933; PID:g474934
A;Superfamily: IGFBP-related protein, CNN type

Query Match       100.0%;  Score 956; DB 2;  Length 349;
Best Local Similarity  100.0%;
Matches  172; Conservative  0; Mismatches  0; Indels  0; Gaps  0;

Qy        1 ALAAYRLEDTFGPDPTMIRANCLVQTTEWSACSKTCGMGISTRVTNDNASCRLEKQSRLC 60
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      178 ALAAYRLEDTFGPDPTMIRANCLVQTTEWSACSKTCGMGISTRVTNDNASCRLEKQSRLC 237

Qy       61 MVRPCEADLEENIKKGKKCIRTPKISKPIKFELSGCTSMKTYRAKFCGVCTDGRCCTPHR 120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      238 MVRPCEADLEENIKKGKKCIRTPKISKPIKFELSGCTSMKTYRAKFCGVCTDGRCCTPHR 297

Qy      121 TTTLPVEFKCPDGEVMKKNMMFIKTCACHYNCPGDNDIFESLYYRKMYGDMA 172
            |||||||||||||||||||||||||||||||||||||||||||||||||||
Db      298 TTTLPVEFKCPDGEVMKKNMMFIKTCACHYNCPGDNDIFESLYYRKMYGDMA 349

RESULT 2
A40578
beta IG-M2 protein precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 06-Mar-1992 #sequence_revision 06-Mar-1992 #text_change 31-Dec-2004
C;Accession: A40578; A53228
R;Brunner, A.; Chinn, J.; Neubauer, M.; Purchio, A.F.
DNA Cell Biol. 10, 293-300, 1991
A;Title: Identification of a gene family regulated by transforming growth factor-beta.
A;Reference number: A40578; MUID:91229699; PMID:2029337
```

RESULT 4
I38069

A;Accession: A40578
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-348 <BRU>
A;Cross-references: UNIPROT:P29268; UNIPARC:UPI00000028AEF; GB:M80263; NID:g201945; PIDN:
R;Ryseck, R.P.; Macdonald-Bravo, H.; Mattei, M.G.; Bravo, R.
R;Title: Structure, mapping, and expression of fisp-12, a growth factor-inducible gene e
Cell Growth Differ. 2, 225-233, 1991
A;Reference number: A53228; MUID:91363290; PMID:1888698
A;Accession: A53228
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-160,'K',162-348 <RYS>
A;Cross-references: UNIPARC:UPI00000003FD12; GB:M70641; NID:g193313; PIDN:AAA37627.1; PID
C;Genetics:
A;Gene: fisp-12
C;Superfamily: IGFBP-related protein, CNN type

Query Match 97.7%; Score 934; DB 2; Length 348;
Best Local Similarity 95.9%; Pred. No. 8.8e-75;
Matches 165; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ALAAYRLEDTFGPDPTMIRANCLVQTTEWSACSKTCGMGISTRVTNDNASCRLEKQSRLC 60
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 177 ALAAYRLEDTFGPDPTMMRANCLVQTTEWSACSKTCGMGISTRVTNDNTFCRLEKQSRLC 236

Qy 61 MVRPCEADLEENIKKGKKCIRTPKISKPIKFELSGCTSMKTYRAKFCGVCTDGRCCTPHR 120
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 237 MVRPCEADLEENIKKGKKCIRTPKIAKPVKFELSGCTSVKTYRAKFCGVCTDGRCCTPHR 296

Qy 121 TTTLPVEFKCPDGEVMKKNMMFIKTCACHYNCPGDNDIFESLYYRKMYGDMA 172
        |||||||||||||||||||||||||||||||||||||||||||||||||||
Db 297 TTTLPVEFKCPDGEIMKKNMMFIKTCACHYNCPGDNDIFESLYYRKMYGDMA 348

RESULT 3
S20078

S20078
NOV protein - chicken
C;Species: Gallus gallus (chicken)
C;Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 31-Dec-2004
C;Accession: S20078
R;Joliot, V.; Martinerie, C.; Dambrine, G.; Plassiart, G.; Brisac, M.; Crochet, J.; Perb
Mol. Cell. Biol. 12, 10-21, 1992
R;Title: Proviral rearrangements and overexpression of a new cellular gene (nov) in myel
A;Reference number: S20078; MUID:92107157; PMID:1309586
A;Accession: S20078
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-351 <JOL>
A;Cross-references: UNIPROT:P28686; UNIPARC:UPI00001303BC; EMBL:X59284; NID:g63702; PIDN
C;Genetics:
A;Gene: NOV
C;Superfamily: IGFBP-related protein, CNN type

Query Match 57.2%; Score 546.5; DB 2; Length 351;
Best Local Similarity 59.7%; Pred. No. 1e-40;
Matches 95; Conservative 23; Mismatches 40; Indels 1; Gaps 1;

Qy 1 ALAAYRLEDTFGPDPTMIRANCLVQTTEWSACSKTCGMGISTRVTNDNASCRLEKQSRLC 60
        | ||||||||||| :||||||||||||||| ||: | |: ::|
Db 181 AMAAYRQEATLGIDVSDSSANCIEQTTEWSACSKSCGMGFSTRVTNRQQCEMVKQTRLC 240

Qy 61 MVRPCEADLEENIKKGKKCIRTPKISKPIKFELSGCTSMKTYRAKFCGVCTDGRCCTPHR 120
        ||||| :|| | | ||||| :| ||||| ||||||| ||:||: |:|:| ||||
Db 241 MVRPCENE-EPSDKGKKKCCIQTKKSMKAVRFEYKNCTSVQTYKPRYCGLCNDGRCCTPHN 299

Qy 121 TTTLPVEFKCPDGEVMKKNMMFIKTCACHYNCPGDNDIF-ESLYYRKMYGDMA 172
        |||||| ||| || | ::|::| :||||||| | ::|
Db 300 TKTIQVEFRCPQGKFLKKPMLLINTCVCHGNCPQSNNAF 338

RESULT 5
A35669

gene novH protein - human
C;Species: Homo sapiens (man)
C;Date: 17-May-1996 #text_change 31-Dec-2004
C;Accession: I38069
R;Martinerie, C.; Huff, V.; Joubert, I.; Badzioch, M.; Saunders, G.; Strong, L.; Perbal,
Oncogene 9, 2729-2732, 1994
R;Title: Structural analysis of the human nov proto-oncogene and expression in Wilms tum
A;Reference number: I38069; MUID:94336229; PMID:7520150
A;Accession: I38069
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-357 <RES>
A;Cross-references: UNIPROT:P48745; UNIPARC:UPI0001303BE; EMBL:X78351; NID:g587422; PID:
C;Genetics:
A;Gene: novH
A;Introns: 28/3; 104/1; 188/1; 259/3
C;Superfamily: IGFBP-related protein, CNN type
F;203-250/Domain: thrombospondin type 1 repeat homology <THR1>

Query Match 54.3%; Score 519; DB 2; Length 357;
Best Local Similarity 54.7%; Pred. No. 2.7e-38;
Matches 94; Conservative 25; Mismatches 51; Indels 2; Gaps 2;

Qy 2 LAAYRLEDTFGPDPTMIRANCLVQTTEWSACSKTCGMGISTRVTNDNASCRLEKQSRLCM 61
        |||| :|| ||||| |:|||| ||||||||| |||: |: ||:||:| |::|:|
Db 186 LAAYRPEATLGVEVSDSSVNCIEQTTEWTACSKSCGMGFSTRVTNRQCEMLKQTRLCM 245

Qy 62 VRPCEADLEE-NIKKGKKCIRTPKISKPIKFELSGCTSMKTYRAKFCGVCTDGRCCTPHR 120
        |||| | | ||| |||| || |||| ||||||| || ||: | |:| ||||||
Db 246 VRPCEQPEQPTDKKGKKCCLRTKKSLKAIHLQFKNCTSLHTYKPRFCGVCSDGRCCTPHN 305

Qy 121 TTTLPVEFKCPDGEVMKKNMMFIKTCACHYNCPGDNDIF-ESLYYRKMYGDM 171
        ||||||| ||| || | ::|::| :||||||| | ::|
Db 306 TKTIQAEFQCSPGQIVKKPVMVIGTCTCHTNCPKNNEAFLQELELKTTRGKM 357

gene CYR61 protein precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 28-Sep-1990 #sequence_revision 18-Nov-1992 #text_change 31-Dec-2004
C;Accession: A35669; I48319; S16446
R;O'Brien, T.P.; Yang, G.P.; Sanders, L.; Lau, L.F.
Mol. Cell. Biol. 10, 3569-3577, 1990
R;Title: Expression of cyr61, a growth factor-inducible immediate-early gene.
A;Reference number: A35669; MUID:90287146; PMID:2355916
A;Accession: A35669
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-379 <OAB>
A;Cross-references: UNIPROT:P18406; UNIPARC:UPI000002DFF; GB:M32490; NID:g192909; PIDN..
R;Latinkic, B.V.; O'Brien, T.P.; Lau, L.F.
Nucleic Acids Res. 19, 3261-3267, 1991
R;Title: Promoter function and structure of the growth factor-inducible immediate early
A;Reference number: I48319; MUID:91288203; PMID:2062642
A;Accession: I48319
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-379 <RES>
A;Note: the authors did not translate the codon for residue 108
A;Note: the authors translated the codon GAT for residue 337 as Gln
A;Accession: A35669
C;Genetics:
A;Gene: CYR61
A;Introns: 21/3; 93/1; 208/1; 279/3
C;Superfamily: IGFBP-related protein, CNN type
F;99-166/Domain: von Willebrand factor type C repeat homology <VWC>

Query Match 51.0%; Score 487.5; DB 2; Length 379;
Best Local Similarity 49.4%; Pred. No. 1.7e-35;
Matches 83; Conservative 32; Mismatches 44; Indels 9; Gaps 2;

```
Qy    11 FGPDPTMI-------RANCLVQTTEWSACSKTCGMGISTRVTNDNASCRLEKQSRLCMVR 63
            ||||         |::|:|||||| |||:||||::|:||||||||||:||:::|:||:
Db   209 FGTEPRVLFNPLHAHGQKCIVQTTSWSQCSKSCGTGISTRVTNDNPECRLVKBTRICEVR 268

Qy    64 PCEADLEENIKGKGKKCIRTPKISKPIKFELSGCTSMKTYRAKFCGVCTDGRCCTPHRTTT 123
            || ::|  :|||||||| ::  |:| ::  |||:|:|::|| ||| |:|||||||| : |
Db   269 PCGQPVVSLKGKGKKCSKTKKSPSPVRTYAGCSSVKKYRPKYCGSCVDGRCCTPLQRT 328

Qy   124 LPVEFKCPDGEVMKKGNMMFIKTCACHYNCPGDNDIFESLYYRKMYGDM 171
            :  :||| || ::||| ||| :|| | ||| |: |:  |::|
Db   329 VKMRFRCEDGEMFSKGNVMMIQSCKCNYNCPHPNEASFRLY--SLFNDI 374
```

RESULT 6
A41428
CEF-10 protein precursor - chicken
C;Species: Gallus gallus (chicken)
A;Residues: 1-375 <SIM>
A;Molecule type: mRNA
A;Status: preliminary
A;Accession: A41428
A;Reference number: A41428
A;Title: Identification of a phorbol ester-repressible v-src-inducible gene.
A;Experimental source:
R;Simmons, D.L.; Levy, D.B.; Yannoni, Y.; Erikson, R.L.
Proc. Natl. Acad. Sci. U.S.A. 86, 1178-1182, 1989
A;Accession: A41428; MUID:89145206; PMID:2537491
A;Cross-references: UNIPROT:P13336; UNIPARC:UPI000012748; GB:J04496; NID:g211435; PIDN:
C;Date: 03-Apr-1992 #sequence_revision 03-Apr-1992 #text_change 31-Dec-2004
C;Superfamily: IGFBP-related protein, CNN type

Query Match   50.2%; Score 479.5; DB 2; Length 375;
Best Local Similarity   51.3%; Pred. No. 8.3e-35;
Matches 81; Conservative 27; Mismatches 45; Indels   5; Gaps   2;

```
Qy    11 FGPDP------TMIRANCLVQTTEWSACSKTCGMGISTRVTNDNASCRLEKQSRLCMVRPCEA 67
            ||||       ::|:|||||||||||||||||||||||||||||||:||:::|:||:
Db   210 FGSEPQSRAFENPKCIVQTTSWSQCSKSCGTGISTRVTNDNPDCKLIKETRICEVRPCCQ 269

Qy    68 DLEENIKGKGKKCIRTPKISKPIKFELSGCTSMKTYRAKFCGVCTDGRCCTPHRTTTLPVE 127
            :  :|||||||| ::  |:| ::  |||:|:|::|| ||| |:||||||||
Db   270 PSYASLKGKGKKCKTKTKKSPSPVRTYAGCSSVKKYRPKYCGSCVDGRCCTPQQTRTVKIR 329

Qy   128 FKCPDGEVMKKGNMMFIKTCACHYNCPGDNDIFESLYYR 165
            |:|||| ::||| ||| :|| | ||| |: |:  |::|
Db   330 FRCDDGEFFKSVMMIQSCRCNYNCPHANEAYP--FYR 365
```

RESULT 7
T21371
hypothetical protein F25H8.3 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
A;Accession: T21371; T24896
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
R;Gajaddty, S.
submitted to the EMBL Data Library, February 1996
A;Reference number: Z19413
A;Cross-references: UNIPROT:Q19791; UNIPARC:UPI00000?CF95; EMBL:Z69360; PIDN:CAA93287.1,
A;Experimental source: clone F25H8
A;Molecule type: DNA
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Accession: T24896
A;Reference number: Z19949
submitted to the EMBL Data Library, February 1996
R;Gajaddty, S.
A;Experimental source: clone T13H10
A;Cross-references: UNIPARC:UPI00000?CF95; EMBL:Z69361; PIDN:CAA93288.1; GSPDB:GN000022;
A;Molecule type: DNA
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-2165 <WI2>
A;Gene: CESP:F25H8.3
A;Map position: 4
A;Introns: 31/1; 52/1; 135/2; 193/3; 216/1; 266/1; 495/2; 547/3; 584/3; 634/2; 744/1; 81

Query Match   12.1%; Score 116; DB 2; Length 2165;
Best Local Similarity   21.3%; Pred. No. 0.037;
Matches 50; Conservative 31; Mismatches 52; Indels 102; Gaps 14;

```
Qy    15 PTMIR----ANCLVQTT--EWSACSKTCGMGISTRVT-----NDNAS------ 50
           |:  ||    ||||:||    ||:||||:|||||||||      ::
Db  1798 PTSIRECDTDSNCPYEWVPGDWQTCSKSCGEGVQTREVRCRRKINFNSTIPIIFMLEDEPA 1857

Qy    51 -----CRL---EKQSRLCMVRPCEADLE----------------ENIKGGK-KCIRTPKISK 87
                ||:      ::|||||||||:|                  |: : ::| :
Db  1858 VPKEKCELFPKPNESQTCELNPCDSEFKNSFGPWGECSKNCGQGIRRRVKCV----AND 1913

Qy    88 PIKFELSGCTSMKTYRAKFCGVCTDGRCCTP----------------------------- 118
           |||||||||||||||||||||||||||||:
Db  1914 GRRVERVKCTTKKPRRTQYC----FERNCLPSTCOELKSQONVKAKDGNYTILLDGFTIEI 1969

Qy   119 --HR-TTTLP-----VEFKCPDGEVMKKGNMMFIKTC------------ACHYNCPGDND 157
             |: :  ||       :||||||||||||||||||||             |||||||||
Db  1970 YCHRMNSTIPKAYLNVNPRTNFAEVYGKDLIYPHTCPFNGDRNDSCH--CSEDGD 2022
```

RESULT 8
T18856
angiogenesis inhibitor homolog - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
A;Accession: T18856
A;Molecule type: DNA
A;Residues: 1-1444 <WIL>
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Reference number: Z19031
submitted to the EMBL Data Library, July 1995
R;McMurray, A.
A;Experimental source: clone C02B4
A;Cross-references: UNIPROT:Q8MYA8; UNIPARC:UPI000007?5CEB; EMBL:Z50004; PIDN:CAA90293.1,
A;Accession: T24653
A;Reference number: Z19917
submitted to the EMBL Data Library, July 1995
R;McMurray, A.
A;Experimental source: clone C02B4
A;Molecule type: DNA
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-1444 <WI2>
A;Cross-references: UNIPARC:UPI000007?5CEB; EMBL:Z50006; PIDN:CAA90302.1; GSPDB:GN000028;
A;Gene: CESP:C02B4.1
C;Genetics:
A;Map position: X
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004

Query Match   11.2%; Score 107; DB 2; Length 1444;
Best Local Similarity   26.1%; Pred. No. 0.16;
Matches 29; Conservative 15; Mismatches 45; Indels 22; Gaps   3;

```
Qy    27 TEWSACSKTCGM-GISTR---VTNDNASCRLEKQSRLCMVRPCEADLEENIKKGKCIRT 82
           |:||:|||:|||  ||||    :|:|::|  :::: |:  :
Db  1072 SDWSSCSKSCGQDGIOTRQKLCLFNNAECSSYAESRRCKDLPSCSSISSGRTISENGFDA 1131

Qy    83 PKISKPIKFELSGCTSMKTYRAKFCGV----------------CTDGRC 115
           |:: | ||||||||||||||||||||                 |||||
Db  1132 PRWSENWSSWSACSCFSLTSTRRRFCQVVDPTVQGFCAGAILEQIPCAPGSC 1182
```

RESULT 9
T18397
protein CTRP - malaria parasite (Plasmodium falciparum)
C;Species: Plasmodium falciparum
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T18397
R;Trottein, F.; Triglia, T.; Cowman, A.F.

Mol. Biochem. Parasitol. 74, 129-142, 1995
R;Tomley, F.M.; Clarke, L.E.; Kawazoe, U.; Dijkema, R.; Kok, J.J.
A;Title: Molecular cloning of a gene from Plasmodium falciparum that codes for a protein
A;Reference number: 218926; MUID:96360471; PMID:8719155
A;Accession: T18397
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-2098 <TRO>
A;Cross-references: UNIPARC:UPI000008040C; EMBL:U34363; NID:g1098897; PI

Query Match   10.7%;   Score 102.5; DB 2; Length 2098;
Best Local Similarity   23.8%;   Pred. No. 0.55;
Matches 40; Conservative 21; Mismatches 52; Indels 55; Gaps 10;

```
Qy    28 EWSACSKTCGMGISTRVTNDNA-----------SCRLEKQSRL--CMVRPCE-----ADLEENIKK- 75
Db  1586 EWSECSATCGEGIRVR-NRDNSLDNDDKCKLFNSTEMEACNIQECDDNNVDICEDIGEW 1644

Qy    76 ----GKKC--------IRTPKISKPIKFELSGGCTSMKTYRAKFCG-----VCTDGRC- 115
Db  1645 SDWSGCSKTCGYSTRSRTFTILPEYIGEYPNCKIFERSETEVCARFIPACSDENCFEWEEW 1704

Qy   116 ------CTPHRTTLPVEFKCPDGEVMKKNMMFIKTCACHYNCPGDND 157
Db  1705 NEWSSPCSPRK-------RVQKARVLKKDDVIISS---------GDNN 1736
```

RESULT 10
A38152
F-spondin - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
R;Klar, A.; Baldassare, M.; Jessell, T.M.
Cell 69, 95-110, 1992
A;Accession: A38152
A;Title: F-spondin: a gene expressed at high levels in the floor plate encodes a secrete
A;Reference number: A38152; MUID:92208952; PMID:1555244
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-807 <KLA>
A;Cross-references: UNIPROT:P35446; UNIPARC:UPI00000012AC71; GB:M88469; NID:g204176; PIDN:

A;Note: sequence extracted from NCBI backbone (NCBIN:90877, NCBIP:90878)
A;Superfamily: F-spondin; thrombospondin type 1 repeat homology
F;48-218/Domain: thrombospondin type 1 repeat homology <THR2>
F;238-296/Domain: thrombospondin type 1 repeat homology <THR3>
F;309-371/Domain: thrombospondin type 1 repeat homology <THR4>
F;372-432/Domain: thrombospondin type 1 repeat homology <THR1>
F;433-493/Domain: thrombospondin type 1 repeat homology <THR5>
F;494-556/Domain: thrombospondin type 1 repeat homology <THR6>
F;560-610/Domain: thrombospondin type 1 repeat homology

Query Match   10.6%;   Score 101.5; DB 2; Length 807;
Best Local Similarity   24.7%;   Pred. No. 0.28;
Matches 42; Conservative 19; Mismatches 46; Indels 63; Gaps 10;

```
Qy    20 ANCLV-QTTEWSACSKTCGMGISTR----------VTNDNASCRLE-KQSRLCMVRPCE----- 66
Db   557 SSCLVTEWGEWDDCSATCGMGMKKRHRMVKMSPADGSMCKAETSQAEKCMMPECHTIPCL 616

Qy    67 -------------ADLEENIKKGKKKCIRTPKISKPIKFELSG 95
Db   617 LSPWSEWSDCSVTCGKGMRTRQRMLKSLAELGDCNEDLEQAEKCM-LPEC--PIDCSLSE 673

Qy    96 CTSMKTYRAKFCGVCTDGRCCTPH----RTTLLPVE----FKCPDGEVMKK 138
Db   674 WSQWSECN-KSCCG---------KGHMIRTIQMEPQFGGAPCPETVQRKK 714
```

RESULT 11
A45638
immunodominant microneme protein Etp100 - Eimeria tenella
C;Species: Eimeria tenella
C;Date: 22-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C;Accession: A45638
R;Tomley, F.M.; Clarke, L.E.; Kawazoe, U.; Dijkema, R.; Kok, J.J.
Mol. Biochem. Parasitol. 49, 277-288, 1991
A;Title: Sequence of the gene encoding an immunodominant microneme protein of Eimeria ter
A;Reference number: A45638; MUID:92131064; PMID:1775171
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-712 <TOM>
A;Cross-references: UNIPROT:O43981; UNIPARC:UPI000007B8B2; GB:AF032905; GB:M73495; NID:g2
A;Note: sequence extracted from NCBI backbone (NCBIN:77752, NCBIP:77756)
A;Superfamily: von Willebrand factor type A repeat homology <VWA1>
F;48-218/Domain: thrombospondin type 1 repeat homology <THR1>
F;309-371/Domain: thrombospondin type 1 repeat homology <THR2>
F;372-432/Domain: thrombospondin type 1 repeat homology <THR3>
F;433-493/Domain: thrombospondin type 1 repeat homology <THR4>
F;494-556/Domain: thrombospondin type 1 repeat homology <THR5>
F;560-610/Domain: thrombospondin type 1 repeat homology <THR6>

Query Match   10.4%;   Score 99; DB 2; Length 712;
Best Local Similarity   24.0%;   Pred. No. 0.41;
Matches 47; Conservative 19; Mismatches 66; Indels 64; Gaps 11;

```
Qy    14 DPTMIRANCLVQTTEWSACSKTCGMGISTRVTN-----DNA-----IRTPKISK 87
Db   429 NPCPIDATC-GEWTEVSACSRTCGGTQERKREPWLDNAQHGGRTC-MEQYPDGPISVRE 486

Qy    88 PIKFELSGGCTSMKTYRAKFCGVC---------TDGRCCTPHRTTTLPVEFKCPDGEVMKKNM 140
Db   487 CNTQPCPVDEVVGDWEDWGQCSEQCGGGKRTRNRGPSKQEAMFGGKTVAQNAELPEGK 546

Qy   141 MFIKTCA--CHYNCPG 154
Db   547 IEVVQEEGCNEVP-------CGPCTLPFSEWTECESCSGHRTRESAVAPDYTD-RMCSGDT 599

Qy        -----QSRLEK--------SCRLEK-----
Db   600 HEVQSCEEYCSQNAGG 615
```

RESULT 12
A47723
F-spondin precursor - African clawed frog
C;Species: Xenopus laevis (African clawed frog)
C;Date: 27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change 09-Jul-2004
C;Accession: A47723
R;Ruiz i Altaba, A.; Cox, C.; Jessell, T.M.; Klar, A.
Proc. Natl. Acad. Sci. U.S.A. 90, 8268-8272, 1993
A;Title: Ectopic neural expression of a floor plate marker in frog embryos injected with
A;Reference number: A47723; MUID:93376785; PMID:8367492
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-803 <RUI>
A;Cross-references: UNIPROT:P35447; UNIPARC:UPI00000012AC72; GB:L09123; NID:g409244; PIDN:
A;Superfamily: F-spondin; thrombospondin type 1 repeat homology
F;435-489/Domain: thrombospondin type 1 repeat homology <THR2>
F;607-662/Domain: thrombospondin type 1 repeat homology <THR1>

Query Match   10.4%;   Score 99; DB 2; Length 803;
Best Local Similarity   26.8%;   Pred. No. 0.46;
Matches 38; Conservative 18; Mismatches 64; Indels 22; Gaps 6;

```
Qy    23 LVQTTEWSACSKTCGMG--ISTRVTN-----DNASCRLEKQSRLCMVRPCE-----ADLEEN 72
Db   667 LTEWSYWSECNKSCGKGHMIRTRMITMEPQFGGAVCPETVQRKCRLRKCQKSSGNERRH 726

Qy    73 IKKGKKCIRTPKISKPIKFELSGCTSMKTYRA-----KFCGVCTDGRCCTPHRTTTLPVE 127
Db   727 LKDAREKRRSEKIKEDSDGEQYPVCKMKPWTAWTECTKFCGGGIQERFMTVKRFKSSQF 786

Qy   128 FKCPDGEVMKKNMMFIKTCACH 149
```

```
Db

RESULT 13
A47437

787 TSCKD----KKE---IRACNVH 801

LDL-receptor-related protein - Caenorhabditis elegans
A47437
C;Species: Caenorhabditis elegans
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
R;Yochem, J.; Greenwald, I.
C;Accession: A47437; S27801; T21547
R;Yochem, J.; Greenwald, I.
A;Title: A gene for a low density lipoprotein receptor-related protein in the nematode C
Proc. Natl. Acad. Sci. U.S.A. 90, 4572-4576, 1993
A;Reference number: A47437; MUID:93281621; PMID:8506301
A;Accession: A47437
A;Molecule type: DNA
A;Residues: 1-4753 <YOC>
A;Cross-references: UNIPROT:Q04833; UNIPARC:UPI000013C4B5; GB:M96150; NID:g156359; PIDN:
R;Yochem, J.; Greenwald, I.
C;Note: nucleotide sequence not given; translation not complete in this paper
submitted to the EMBL Data Library, July 1992
A;Description: A gene for an LDL receptor-related protein (LPR) in the nematode C.elegan
A;Reference number: S27801
A;Accession: S27801
A;Molecule type: DNA
A;Residues: 1-4753 <YO2>
A;Cross-references: UNIPARC:UPI000013C4B5; EMBL:M96150; NID:g156359; PIDN:AAA28105.1; PI
R;Wilkinson, J
submitted to the EMBL Data Library, June 1996
A;Reference number: Z19439
A;Accession: T21547
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-4753 <WIL>
A;Cross-references: UNIPARC:UPI000013C4B5; EMBL:Z73907; PIDN:CAA98124.1; GSPDB:GN00019;
C;Genetics:
C;Experimental source: clone F29D11
C;Keywords: tandem repeat; transmembrane protein
C;Superfamily: alpha-2-macroglobulin receptor; EGF homology; LDL receptor ligand-binding
A;Map position: 1
A;Introns: 31/1; 88/1; 132/1; 172/3; 219/1; 298/1; 463/2; 526/2; 585/3; 780/2; 874/2; 97
15/1
A;Gene: LPR
C;Genetics:
A;Gene: LPR
F;53-87/Domain: LDL receptor ligand-binding repeat homology <LDL1>
F;92-131/Domain: LDL receptor ligand-binding repeat homology <LDL2>
F;138-175/Domain: LDL receptor ligand-binding repeat homology <LDL3>
F;182-218/Domain: LDL receptor ligand-binding repeat homology <LDL4>
F;223-257/Domain: LDL receptor ligand-binding repeat homology <LDL5>
F;262-297/Domain: LDL receptor ligand-binding repeat homology <LDL6>
F;302-336/Domain: EGF homology <EGF1>
F;1054-1095/Domain: LDL receptor ligand-binding repeat homology <LDL7>
F;1101-1138/Domain: LDL receptor ligand-binding repeat homology <LDL8>
F;1146-1182/Domain: LDL receptor ligand-binding repeat homology <LDL9>
F;1187-1223/Domain: LDL receptor ligand-binding repeat homology <LDL10>
F;1228-1263/Domain: LDL receptor ligand-binding repeat homology <LDL11>
F;1270-1307/Domain: LDL receptor ligand-binding repeat homology <LDL12>
F;1313-1350/Domain: LDL receptor ligand-binding repeat homology <LDL13>
F;1359-1396/Domain: LDL receptor ligand-binding repeat homology <LDL14>
F;1441-1475/Domain: EGF homology <EGF>
F;1611-1654/Domain: YWTD-containing repeat homology <YW33>
F;2792-2829/Domain: LDL receptor ligand-binding repeat homology <LDL15>
F;2834-2868/Domain: LDL receptor ligand-binding repeat homology <LDL16>
F;2874-2912/Domain: LDL receptor ligand-binding repeat homology <LDL17>
F;2919-2956/Domain: LDL receptor ligand-binding repeat homology <LDL18>
F;2961-2997/Domain: LDL receptor ligand-binding repeat homology <LDL19>
F;3006-3044/Domain: LDL receptor ligand-binding repeat homology <LDL20>
F;3049-3093/Domain: LDL receptor ligand-binding repeat homology <LDL21>
F;3100-3135/Domain: LDL receptor ligand-binding repeat homology <LDL22>
F;3140-3174/Domain: LDL receptor ligand-binding repeat homology <LDL23>
F;3187-3222/Domain: LDL receptor ligand-binding repeat homology <LDL24>
F;3586-3623/Domain: EGF homology <EGX1>
F;3627-3666/Domain: LDL receptor ligand-binding repeat homology <LDL25>
F;3671-3705/Domain: LDL receptor ligand-binding repeat homology <LDL26>
F;3709-3746/Domain: LDL receptor ligand-binding repeat homology <LDL27>

F;3753-3788/Domain: LDL receptor ligand-binding repeat homology <LDL28>
F;3793-3830/Domain: LDL receptor ligand-binding repeat homology <LDL29>
F;3833-3871/Domain: LDL receptor ligand-binding repeat homology <LDL30>
F;3878-3912/Domain: LDL receptor ligand-binding repeat homology <LDL31>
F;3917-3951/Domain: LDL receptor ligand-binding repeat homology <LDL32>
F;3959-3995/Domain: LDL receptor ligand-binding repeat homology <LDL33>
F;4000-4040/Domain: LDL receptor ligand-binding repeat homology <LDL34>
F;4049-4083/Domain: LDL receptor ligand-binding repeat homology <LDL35>
F;4092-4130/Domain: EGF homology <EGF2>
F;4343-4386/Domain: LDL receptor YWTD-containing repeat homology <YW38>

Qy         Query Match      10.1%;  Score 97;  DB 1;  Length 4753;
           Best Local Similarity  21.8%;  Pred. No. 3.6;
Matches    46;  Conservative  17;  Mismatches  68;  Indels  80;  Gaps  10;

Qy      15 PTMIRANCLVQTTEWSACSKTCGMGISTRVTNDNASCR---LEKQSRLCM---------- 61
Db    1019 PNELEAKC---------------ACRGGFMINKEN-NHSCQXDPAEKIEQLCSSNSTQFQCKN 1065

Qy      62 ------VRPCEADLEENIKKGKKCI--------------RTPKISKPIKFELSGCT 97
Db    1066 GRCIPKEWKCDGENDCLDBSDEIDEKGDKCFHETECAENTIKCRNTKKCIPAQYGCDGDN 1125

Qy      98 SMKTYRAKFCGVCTDGR----C------CTPHRTTTLPVEFKCP------DGEVMKKNMMF 142
Db    1126 DCGDYSDEDVKYCKDGQKPVCAAKFQCDNHR--CIPEQWKCDSDNDCGDGSDEKLEMCG 1183

Qy     143 IKTCAC------------------HYNCPGDNIFE 160
Db    1184 NATCAANQFSCANGRCIPIYWLCDGDNDCYD 1214


RESULT 14
T29247
hypothetical protein F09F9.4 - Caenorhabditis elegans
T29247
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
R;Minx, P.; Hawkins, J.
submitted to the EMBL Data Library, November 1995
C;Description: The sequence of C. elegans cosmid F09F9.
A;Reference number: Z20594
A;Accession: T29247
A;Molecule type: DNA
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-654 <MIN>
A;Cross-references: UNIPROT:Q19284; UNIPARC:UPI00000755SE; EMBL:U40958; PIDN:AAA81764.1,
C;Genetics:
A;Gene: CESP:F09F9.4
A;Introns: 89/3; 138/3; 192/3; 260/1; 312/1; 400/2; 445/3; 496/1; 523/1; 558/2; 596/2

Query Match      10.1%;  Score 96.5;  DB 2;  Length 654;
Best Local Similarity  29.2%;  Pred. No. 0.63;
Matches    35;  Conservative  16;  Mismatches  48;  Indels  21;  Gaps  7;

Qy      27 TEWSACSKTCGMGISTRVTNDNASCRLEKQSRLC---MVRPCEADLEENIKKGKKCIRTP 83
Db     323 SEWSACSETCGSGRQRRVRFCNEP--VPKRSKYCDGPLIETQECTL-------TKC---P 370

Qy      84 KISKPIKFELS---GCTSMKTYRAKFCGVCTDGRCCTPHRTTTLPV--EFKCPDGEVMKK 138
Db     371 EAMMPQSLSTNCSCGC-ALSLEASSFFASSRHSRMCEGNQTWTLPKMDGFKIADFTIRKQ 429


RESULT 15
T14764
hypothetical protein DKFZp434H204.1 - human (fragment)
T14764
C;Species: Homo sapiens (man)
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
A;Accession: T14764
R;Wambutt, R.; Heubner, D.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
submitted to the Protein Sequence Database, August 1999
A;Reference number: Z18181
```

A;Accession: T14764
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-898 <WAM>
A;Cross-references: UNIPROT:Q9UFZ4; UNIPARC:UPI000006D6B6; EMBL:AL110226
A;Experimental source: adult testis; clone DKFZp434H204
C;Genetics:
A;Note: DKFZp434H204.1

```
Query Match    10.1%;  Score 96.5;  DB 2;  Length 898;
Best Local Similarity   28.2%;  Pred. No. 0.85;
Matches  37;  Conservative  12;  Mismatches  47;  Indels  35;  Gaps  7;

Qy    12 GP--DPTMIRANCLVQTTEWSACSKTCGMG-------ISTRVTNDNASCRLEKQSRLCMV  62
         ||  |::|||   | |:|| |||||| || :           :  ||  :: ::|||
Db   614 GPPADPLVVR-NASWQAGNWSECSTTCGLGAVWRPVRCSSGRDEDCAPAGRPQPARRCHL 672

Qy    63 RPCEADLEENIKKGKKCCIRTPKISKPIKFELSGCTSMKTYRAKFCGVCTDGRCCTPHRTT 122
         |||          |:  :     :    :  : |:||:                 :
Db   673 RPCATWHSGN--WSKCSRS---------CGGGSSVRDVQ------CVDTRDLRPLR--    711

Qy   123 TLPVEFKCPDG 133
            |  |:|| |
Db   712 ----PFHCQPG 718
```

Search completed: January 9, 2006, 11:19:58
Job time : 41 secs

Protein Sequence Searches - February 2005

All of the sequence databases on ABSS have recently been updated.

- Please note that the curators of the UniProt database have purged some temporary accession numbers from the most recent version of UniProt. These sequences have been assigned new permanent accession numbers. The new UniProt record may not contain the previous temporary accession number.

- If you encounter an accession number from an older search run against UniProt (results.file extension .rup) that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein Archive database (UniPARC) at:

    http://www.pir.uniprot.org/database/archive.shtml

If you have any questions regarding this information or your results, please contact any STIC searcher.

When submitting sequence search results for scanning into IFW, please include a copy of this attachment to assist any future Examiners or members of the public who may encounter UniProt temporary accession numbers.

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OM protein - protein search, using sw model

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GenCore version 5.1.6

Run on: January 9, 2006, 11:11:01 ; Search time 160 Seconds
(without alignments)
758.443 Million cell updates/sec

Title: US-09-461-646-4
Perfect score: 956
Sequence: 1 ALAAYRLEDTFGPDPTMIRA.........PGDNDIFESLYYRKMYGDMA 172

Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database : UniProt_05.80:*
           1: uniprot_sprot:*
           2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result NO.	Score	% Query Match	Length	DB	ID	Description
1	956	100.0	275	2	Q6LCY0_HUMAN q6lcy0	homo sapiens
2	956	100.0	349	2	CTGF_HUMAN p29279	homo sapiens
3	956	100.0	349	1	CTGF_HUMAN P29279	homo sapien
4	956	100.0	349	2	Q6FH18_HUMAN q6fh18	homo sapien
5	943	98.6	349	2	Q5M8T4_HUMAN q5m8t4	homo sapien
6	938	98.1	349	2	CTGF_PIG o97765	sus scrofa
7	937	98.0	349	2	CTGF_BOVIN o18739	bos taurus
8	934	97.7	349	1	CTGF_RAT o19113	sus scrofa
9	934	97.7	347	2	Q9I1e9_RAT q9i1e9	rattus norv
10	934	97.7	348	1	CTGF_MOUSE Q53Y70	rattus norv
11	925	96.8	344	2	Q98TQ8_CHICK P29268	mus musculu
12	898	93.9	343	2	Q42607_XENLA q42607	xenopus lae
13	898	93.9	343	2	Q5O5L5_XENLA q5o5l5	xenopus lae
14	894	93.5	343	2	Q5BKN7_XENTR q5bkn7	xenopus tro
15	893	93.4	347	2	Q9PT80_NOTVI q9pt80	notophthalm
16	838	87.7	345	2	Q5RI33_BRARE q5ri33	brachydanio
17	802.5	83.9	357	2	Q4SC24_TETNG q4sc24	tetraodon n
18	692	72.4	125	2	Q862T0_BOVIN q862t0	bos taurus
19	662	69.2	119	2	Q920W6_MUSSI q920w6	mus spicile
20	662	69.2	119	2	Q91V29_MOUSE q91v29	mus musculu
21	566	59.2	113	2	Q92164_RAT q92164	rattus norv
22	547.5	57.3	353	1	NOV_COTJA P42642	coturnix co
23	546.5	57.2	351	1	NOV_CHICK P28686	gallus gall
24	524.5	54.9	343	2	Q6INN3_XENLA P51609	xenopus lae
25	524.5	54.9	343	1	NOV_XENLA Q6inn3	xenopus lae
26	519.5	54.3	354	1	NOV_MOUSE Q64299	mus musculu
27	519	54.3	357	2	Q61993_HUMAN P48745	homo sapien
28	518.5	54.2	357	2	NOV_HUMAN Q61993	homo sapien
29	506	52.9	351	1	NOV_RAT Q9czq5	rattus norv
30	499	52.2	375	2	Q98TX5_XENLA Q98tx5	xenopus lae
31	498	52.1	375	2	Q5BL74_XENTR Q5bl74	xenopus tro
32	489.5	51.2	379	1	CYR61_RAT Q9ee72	rattus norv
33	488.5	51.1	361	2	Q4RJ69_TETNG q4rj69	tetraodon n
34	488.5	51.1	379	1	CYR61_MOUSE P18406	mus musculu
35	487.5	51.0	379	2	Q9WTM9_RAT q9wtm9	rattus norv
36	487.5	51.0	349	2	Q66HT5_RAT q66ht5	rattus norv
37	485.5	50.8	381	1	CYR61_HUMAN O00622	homo sapien
38	485.5	50.8	381	2	Q6FI18_HUMAN q6fi18	homo sapien
39	479.5	50.2	375	2	CEF10_CHICK P19336	gallus gall
40	479.5	50.2	359	2	Q42ZF1_CHICK q42zf1	gallus gall
41	473.5	49.5	375	1	Q53FA4_HUMAN q53fa4	homo sapien
42	461	48.2	385	2	Q61R79_XENLA q61r79	xenopus lae
43	459	48.0	369	2	Q6NWA0_BRARE q6nwa0	brachydanio
44	459	48.0	400	2	Q6PFI2_BRARE q6pfi2	brachydanio
45	445	46.5	318	2	Q4SH80_TETNG q4sh80	tetraodon n

ALIGNMENTS

RESULT 1
Q6LCY0_HUMAN

ID   Q6LCY0_HUMAN PRELIMINARY;   PRT;   275 AA.
AC   Q6LCY0;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Connective tissue growth factor (Fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=91373462; PubMed=1654338; DOI=10.1083/jcb.114.6.1285;
RA   Bradham D.M., Igarashi A., Potter R.L., Grotendorst G.R.;
RT   "Connective tissue growth factor: a cysteine-rich mitogen secreted by
RT   human vascular endothelial cells is related to the SRC-induced
RT   immediate early gene product CEF-10.";
RL   J. Cell Biol. 114:1285-1294(1991).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RA   Sutter T.R., Guzman K., Dold K.M., Greenlee W.F.;
RT   "Targets for dioxin: genes for plasminogen activator inhibitor-2 and
RT   interleukin-1 beta.";
RL   Science 254:415-418(1991).
RN   [3]
RP   NUCLEOTIDE SEQUENCE.
RA   Cody C.W., Walker N.J., Greenlee W.F., Sutter T.R.;
RL   Submitted (SEP-1994) to the EMBL/GenBank/DDBJ databases.
     EMBL; U14750; AAA75378.1; -; mRNA.
DR   GO; GO:0005576; C:extracellular region; IEA.
DR   GO; GO:0005520; F:insulin-like growth factor binding; IEA.
DR   GO; GO:0001558; P:regulation of cell growth; IEA.
DR   InterPro; IPR006208; Cys_knot.
DR   InterPro; IPR006207; Cys_knot_C.
DR   InterPro; IPR000867; InsI_gro_fac_pr.
DR   InterPro; IPR000884; TSP1.
DR   InterPro; IPR001007; VWF_C.
     Pfam; PF00007; Cys_knot; 1.
     Pfam; PF00219; IGFBP; 1.
     Pfam; PF00090; TSP_1; 1.
     Pfam; PF00093; VWC; 1.
DR   SMART; SM00041; CT; 1.
DR   SMART; SM00209; TSP1; 1.
DR   SMART; SM00214; VWC; 1.
DR   PROSITE; PS01185; CTCK_1; 1.
DR   PROSITE; PS01225; CTCK_2; 1.
DR   PROSITE; PS00121; TSP1; 1.
DR   PROSITE; PS00092; VWFC_1; 1.
DR   PROSITE; PS01208; VWFC_2; 1.
DR   PROSITE; PS50184; VWFC; 1.
FT   NON_TER   1 .

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SQ   SEQUENCE   275 AA;  30476 MW;  332D31C6F4380815 CRC64;

     Query Match
     Best Local Similarity   100.0%;
     Matches 172;  Conservative
                                  Score 956;  DB 2;  Length 275;
                                  100.0%;   Pred. No. 4.4e-81;
                                     0;  Mismatches  0;  Indels  0;  Gaps  0;

Qy        1 ALAAYRLEDTGFGPDPTMIRANCLVQTTEWSACSKTCGMGISTRVTNDNASCRLEKQSRLC  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      104 ALAAYRLEDTGFGPDPTMIRANCLVQTTEWSACSKTCGMGISTRVTNDNASCRLEKQSRLC 163

Qy       61 MVRPCEADLEENIKKGKKCIRTPKISKPIKFELSGGCTSMKTYRAKFCGVCTDGRCCTPHR 120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      164 MVRPCEADLEENIKKGKKCIRTPKISKPIKFELSGGCTSMKTYRAKFCGVCTDGRCCTPHR 223

Qy      121 TTTLPVEFKCPDGEVMKKNMMFIKTCACHYNCPGDNDIFESLYYRKMYGDMA 172
            |||||||||||||||||||||||||||||||||||||||||||||||||||
Db      224 TTTLPVEFKCPDGEVMKKNMMFIKTCACHYNCPGDNDIFESLYYRKMYGDMA 275
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RESULT 2

CTGF_HUMAN
ID   CTGF_HUMAN   STANDARD;   PRT; 349 AA.
AC   P29279; Q96QX2;
DT   01-DEC-1992 (Rel. 24, Created)
DT   01-DEC-1992 (Rel. 24, Last sequence update)
DT   13-SEP-2005 (Rel. 48, Last annotation update)
DE   Connective tissue growth factor precursor (Hypertrophic chondrocyte-
DE   specific protein 24).
GN   Name=CTGF; Synonyms=CCN2, HCS24;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Umbilical vein endothelial cell;
RX   MEDLINE=9207446; PubMed=1654338; DOI=10.1083/jcb.114.6.1285;
RA   Bradham D.M., Igarashi A., Potter R.L., Grotendorst G.R.;
RT   "Connective tissue growth factor: a cysteine-rich mitogen secreted by
RT   human vascular endothelial cells is related to the SRC-induced
RT   immediate early gene product CEF-10.";
RL   J. Cell Biol. 114:1285-1294(1991).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Aorta;
RX   MEDLINE=92073462; PubMed=1293144;
RA   Oemar B.S., Werner A., Garnier J.M., Do D.D., Godoy N., Nauck M.,
RA   Marz W., Rupp J., Pech M., Luescher T.F.;
RT   "Human connective tissue growth factor is expressed in advanced
RT   atherosclerotic lesions.";
RL   Circulation 95:831-839(1997).
RN   [3]
RP   NUCLEOTIDE SEQUENCE [MRNA] (ISOFORM 1).
RA   Li Q.-H., Wang L.-C., Liu L.-J., Dong S.-Z., Wang J.-J., Hu F.,
RA   Wang J., He S.-Q., Dong C.-H., Zhao S.-D., Zhao H.-L.;
RT   "Expression, purification and bio-activity of human connective tissue
RT   growth factor.";
RL   Submitted (SEP-2003) to the EMBL/GenBank/DDBJ databases.
RN   [4]
RP   NUCLEOTIDE SEQUENCE [MRNA] (ISOFORM 1).
RA   Dai W.-J., Jiang H.-C., Fu S.-B.;
RC   TISSUE=Liver;
RT   "Complete mRNA sequence of human connective tissue growth factor.";
RL   Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.
RN   [5]
RP   NUCLEOTIDE SEQUENCE [MRNA] (ISOFORM 1).
RA   Kalnine N., Chen X., Rolfs A., Halleck A., Hines L., Eisenstein S.,
RA   Koundinya M., Raphael J., Moreira D., Kelley T., LaBaer J., Lin Y.,
RA   Phelan M., Farmer A.;
RT   "Cloning of human full-length CDSs in BD Creator(TM) system donor
RT   vector.";
RL   Submitted (OCT-2004) to the EMBL/GenBank/DDBJ databases.
RN   [6]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 1).
RA   Halleck A., Ebert L., Mkoundinya M., Schick M., Eisenstein S.,
RA   Neubert P., Kstrang K., Schatten R., Shen B., Henze S., Mar W.,
RA   Korn B., Zuo D., Hu Y., LaBaer J.;
RT   "Cloning of human full open reading frames in Gateway(TM) system entry
RT   vector (pDONR201).";
RL   Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
RN   [7]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 1).
RC   TISSUE=Chondrocyte;
RX   MEDLINE=20080284; PubMed=10614647; DOI=10.1210/en.141.1.264;
RA   Nakanishi T., Nishida T., Shimo T., Kobayashi K., Kubo T.,
RA   Tamatani T., Tezuka K., Takigawa M.;
RT   "Effects of CTGF/Hcs24, a product of a hypertrophic chondrocyte-
RT   specific gene, on the proliferation and differentiation of
RT   chondrocytes in culture.";
RL   Endocrinology 141:264-273(2000).
RN   [8]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX   MEDLINE=22935763; PubMed=14574404; DOI=10.1038/nature02055;
RA   Mungall A.J., Palmer S.A., Sims S.K., Edwards C.A., Ashurst J.L.,
RA   Wilming L., Jones M.C., Horton R., Hunt S.E., Scott C.E.,
RA   Gilbert J.G.R., Clamp M.E., Bethel G., Milne S., Ainscough R.,
RA   Almeida J.P., Ambrose K.D., Andrews T.D., Ashwell R.I.S.,
RA   Babbage A.K., Bagguley C.L., Bailey J., Banerjee R., Barker D.J.,
RA   Barlow K.F., Bates K., Beare D.M., Beasley H., Beasley O., Bird C.P.,
RA   Blakey S.E., Bray-Allen S., Brook J., Brown A.J., Brown J.Y.,
RA   Burford D.C., Burrill W., Burton J., Carder C., Carter N.P.,
RA   Chapman J.C., Clark S.Y., Clark G., Clee C.M., Clegg S., Cobley V.,
RA   Collier R.E., Collins J.E., Colman L.K., Corby N.R., Coville G.J.,
RA   Culley K.M., Dhami P., Davies J., Dunn M., Earthrowl M.E.,
RA   Ellington A.E., Evans K.A., Faulkner L., Francis M.D., Frankish A.,
RA   Frankland J., French L., Garner P., Garnett J., Ghori M.J.,
RA   Gilby L.M., Gillson C.J., Glithero R.J., Grafham D.V., Grant M.,
RA   Gribble S., Griffiths C., Griffiths M.N.D., Hall R., Halls K.S.,
RA   Hammond S., Harley J.L., Hart E.A., Heath P.D., Heathcott R.,
RA   Holmes S.J., Howden P.J., Howe K.L., Howell G.R., Huckle E.,
RA   Humphray S.J., Humphries M.D., Hunt A.R., Johnson C.M., Joy A.A.,
RA   Kay M., Keenan S.J., Kimberley A.M., King A., Laird G.K., Langford C.,
RA   Lawlor S., Leongamornlert D.A., Leversha M., Lloyd C.R., Lloyd D.M.,
RA   Loveland J.E., Lovell J., Martin S., Mashreghi-Mohammadi M.,
RA   Maslen G.L., Matthews L., McCann O.T., McLaren S.J., McLay K.,
RA   McMurray A., Moore M.J.F., Mullikin J.C., Niblett D., Nickerson T.,
RA   Novik K.L., Oliver K., Overton-Larty E.K., Parker A., Patel R.,
RA   Pearce A.V., Peck A.I., Phillimore B.J.C.T., Phillips S., Plumb R.W.,
RA   Porter K.M., Ramsey Y., Ranby S.A., Rice C.M., Ross M.T., Searle S.M.,
RA   Sehra H.K., Sheridan E., Skuce C.D., Smith S., Smith M., Spraggon L.,
RA   Squares S.L., Steward C.A., Sycamore N., Tamlyn-Hall G., Tester J.,
RA   Theaker A.J., Thomas D.W., Thorpe A., Tracey A., Tromans A., Tubby B.,
RA   Wall M., Wallis J.M., West A.P., White S.S., Whitehead S.L.,
RA   Whittaker H., Wild A., Willey D.J., Wilmer T.E., Wood J.M., Wray P.W.,
RA   Wyatt J.C., Young L., Younger R.M., Bentley D.R., Coulson A.,
RA   Durbin R., Hubbard T., Sulston J.E., Dunham I., Rogers J., Beck S.;
RT   "The DNA sequence and analysis of human chromosome 6.";
RL   Nature 425:805-811(2003).
RN   [9]
RP   FUNCTION.
RL   Endocrinol. 176:R1-R7(2003).
RN   [10]
RP   HEPARIN-BINDING, AND CELL ADHESION.
RX   MEDLINE=22442376; PubMed=12553878; DOI=10.1677/joe.0.176R001;
RA   Ball D.K., Rachfal A.W., Kemper S.A., Brigstock D.R.;
RT   "The heparin-binding 10 kDa fragment of connective tissue growth
RT   factor (CTGF) containing module 4 alone stimulates cell adhesion.";
RL   J. Endocrinol. 176:R1-R7(2003).
-!- FUNCTION: Major connective tissue mitoattractant secreted by
    vascular endothelial cells. Promotes proliferation and
    differentiation of chondrocytes. Mediates heparin- and divalent

CC   cation-dependent cell adhesion in many cell types including
CC   fibroblasts, myofibroblasts, endothelial and epithelial cells.
CC   Enhances fibroblast growth factor-induced DNA synthesis.
CC   -!- SUBUNIT: Monomer.
CC   -!- SUBCELLULAR LOCATION: Found in the extracellular matrix and as a
CC   soluble form (By similarity).
CC   -!- ALTERNATIVE PRODUCTS:
CC   Event=Alternative splicing; Named isoforms=2;
CC   Name=1; Synonyms=Long;
CC   IsoId=P29279-1; Sequence=Displayed;
CC   Name=2; Synonyms=Short;
CC   IsoId=P29279-2; Sequence=VSP_002460;
CC   Note=No experimental confirmation available;
CC   -!- SIMILARITY: Belongs to the CCN family.
CC   -!- SIMILARITY: Contains 1 CTCK (C-terminal cystine knot-like) domain.
CC   -!- SIMILARITY: Contains 1 IGFBP domain.
CC   -!- SIMILARITY: Contains 1 TSP type-1 domain.
CC   -!- SIMILARITY: Contains 1 VWFC domain.
CC   --
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   --
DR   EMBL; M92934; AAA91279.1; -; mRNA.
DR   EMBL; X78947; CAA55544.1; -; mRNA.
DR   EMBL; AY395801; AAQ95223.1; -; mRNA.
DR   EMBL; AY550024; AAS55639.1; -; mRNA.
DR   EMBL; BT019794; AAV38597.1; -; mRNA.
DR   EMBL; BT019795; AAV38598.1; -; mRNA.
DR   EMBL; CR541759; CAG46559.1; -; mRNA.
DR   EMBL; AL354866; CAC44023.1; -; Genomic_DNA.
DR   PIR; A40551; A40551.
DR   HGNC; HGNC:2500; CTGF.
DR   MIM; 121009; -.
DR   Ensembl; ENSG00000118523; Homo sapiens.
DR   GO; GO:0005578; C:extracellular matrix (sensu Metazoa); TAS.
DR   GO; GO:0005886; C:plasma membrane; TAS.
DR   GO; GO:0005520; F:insulin-like growth factor binding; TAS.
DR   GO; GO:0008544; P:epidermis development; TAS.
DR   GO; GO:0009611; P:response to wounding; TAS.
DR   InterPro; IPR006208; Cys_knot.
DR   InterPro; IPR006207; Cys_knot_C.
DR   InterPro; IPR012395; IGFBP_CNN.
DR   InterPro; IPR000867; IGFBP_like.
DR   InterPro; IPR000884; TSP1.
DR   InterPro; IPR001007; VWF_C.
DR   Pfam; PF00007; Cys_knot; 1.
DR   Pfam; PF00219; IGFBP; 1.
DR   Pfam; PF00090; TSP_1; 1.
DR   Pfam; PF00093; VWC; 1.
DR   PIRSF; PIRSF036495; IGFBP_rP_CNN; 1.
DR   SMART; SM00041; CT; 1.
DR   SMART; SM00121; IB; 1.
DR   SMART; SM00209; TSP1; 1.
DR   SMART; SM00214; VWC; 1.
DR   PROSITE; PS01185; CTCK_1; 1.
DR   PROSITE; PS01225; CTCK_2; 1.
DR   PROSITE; PS00222; IGF_BINDING; 1.
DR   PROSITE; PS00092; TSP1; 1.
DR   PROSITE; PS01208; VWFC_1; 1.
DR   PROSITE; PS50184; VWFC_2; 1.
KW   Alternative splicing; Cell adhesion; DNA synthesis;
KW   Extracellular matrix; Glycoprotein; Heparin-binding; Signal.
FT   SIGNAL   1   26
FT   CHAIN   27   349   Potential.
FT   DOMAIN   33   100   IGFBP.
FT   DOMAIN   101   167   VWFC.
FT   DOMAIN   198   243   TSP type-1.
FT   DOMAIN   256   330   CTCK.
FT   REGION   247   349   Heparin-binding.
FT   CARBOHYD   28   28   N-linked (GlcNAc...) (Potential).
FT   CARBOHYD   225   225   N-linked (GlcNAc...) (Potential).
FT   DISULFID   256   293   By similarity.

Query Match   100.0%; Score 956; DB 1; Length 349;
Best Local Similarity 100.0%; Pred. No. 5.6e-81;
Matches 172; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 ALAAYRLEDTFGPDPTMIRANCLVQTTEWSACSKTCGMGISTRVTNDNASCRLEKQSRLC   60
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Db 178 ALAAYRLEDTFGPDPTMIRANCLVQTTEWSACSKTCGMGISTRVTNDNASCRLEKQSRLC 237

Qy   61 MVRPCEADLEENIKKGKKCIRTPKISKPIKFELSGCTSMKTYRAKFCGVCTDGRCCTPHR 120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 238 MVRPCEADLEENIKKGKKCIRTPKISKPIKFELSGCTSMKTYRAKFCGVCTDGRCCTPHR 297

Qy 121 TTTLPVEFKCPDGEVMKKNMMFIKTCACHYNCPGDNDIFESLYRKMYGDMA   172
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Db 298 TTTLPVEFKCPDGEVMKKNMMFIKTCACHYNCPGDNDIFESLYRKMYGDMA   349

RESULT 3

Q6FHL8 HUMAN

ID   Q6FHL8_HUMAN   PRELIMINARY;   PRT;   349 AA.
AC   Q6FHL8;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   CTGF protein.
GN   Name=CTGF;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Halleck A., Ebert L., Mkoundinya M., Schick M., Eisenstein S.,
RA   Neubert P., Kstrang K., Schatten R., Shen B., Henze S., Mar W.,
RA   Korn B., Zuo D., Hu Y., LaBaer J.;
RL   Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; CR541734; CAG46534.1; -; mRNA.
DR   GO; GO:0005576; C:extracellular region; IEA.
DR   GO; GO:0005520; F:insulin-like growth factor binding; IEA.
DR   GO; GO:0001558; P:regulation of cell growth; IEA.
DR   InterPro; IPR006208; Cys_knot.
DR   InterPro; IPR006207; Cys_knot_C.
DR   InterPro; IPR000867; Ins1_gro_fac_pr.
DR   InterPro; IPR000884; TSP1.
DR   InterPro; IPR001007; VWF_C.
DR   Pfam; PF00007; Cys_knot; 1.
DR   Pfam; PF00219; IGFBP; 1.
DR   Pfam; PF00090; TSP_1; 1.
DR   Pfam; PF00093; VWC; 1.
DR   SMART; SM00041; CT; 1.
DR   SMART; SM00121; IB; 1.
DR   SMART; SM00209; TSP1; 1.
DR   SMART; SM00214; VWC; 1.
DR   PROSITE; PS01185; CTCK_1; 1.
DR   PROSITE; PS01225; CTCK_2; 1.
DR   PROSITE; PS00222; IGF_BINDING; 1.
DR   PROSITE; PS00092; TSP1; 1.
DR   PROSITE; PS01208; VWFC_1; 1.
DR   PROSITE; PS50184; VWFC_2; 1.
SQ   SEQUENCE   349 AA; 38129 MW; 8CC699641511188 CRC64;

Query Match   100.0%; Score 956; DB 2; Length 349;
Best Local Similarity 100.0%; Pred. No. 5.6e-81;
Matches 172; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 ALAAYRLEDTFGPDPTMIRANCLVQTTEWSACSKTCGMGISTRVTNDNASCRLEKQSRLC   60
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Db 178 ALAAYRLEDTFGPDPTMIRANCLVQTTEWSACSKTCGMGISTRVTNDNASCRLEKQSRLC 237

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Qy    61 MVRPCEADLEENIKKGKKCIRTPKISKPIKFELSGCTSMKTYRAKFCGVCTDGRCCTPHR 120
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Db   238 MVRPCEADLEENIKKGKKCIRTPKISKPIKFELSGCTSMKTYRAKFCGVCTDGRCCTPHR 297

Qy   121 TTTLPVEFKCPDGEVMKKNMMFIKTCACHYNCPGDNDIFESLYYRKMYGDMA 172
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Db   298 TTTLPVEFKCPDGEVMKKNMMFIKTCACHYNCPGDNDIFESLYYRKMYGDMA 349
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RESULT 4
ID   Q5M8T4_HUMAN PRELIMINARY;   PRT;   349 AA.
AC   Q5M8T4;
DT   10-MAY-2005 (TrEMBLrel. 30, Created)
DT   10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT   10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE   Connective tissue growth factor.
GN   Name=CTGF;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   TISSUE=Peripheral Nervous System;
RX   MEDLINE=22238257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Peripheral Nervous System;
RL   Director MGC Project;
RL   Submitted (DEC-2004) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC087839; AAH87839.1; -; mRNA.
SQ   SEQUENCE 349 AA; 38069 MW; 0ECF84370B357EA95 CRC64;

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Query Match    100.0%;    Score 956;    DB 2;    Length 349;
Best Local Similarity    100.0%;
Matches    172;    Conservative    0;    Mismatches    0;    Indels    0;    Gaps    0;

Qy     1 ALAAYRLEDTFGPDPTMIRANCLVQTTEWSACSKTCGMGISTRVTNDNASCRLEKQSRLC 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   178 ALAAYRLEDTFGPDPTMIRANCLVQTTEWSACSKTCGMGISTRVTNDNASCRLEKQSRLC 237

Qy    61 MVRPCEADLEENIKKGKKCIRTPKISKPIKFELSGCTSMKTYRAKFCGVCTDGRCCTPHR 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   238 MVRPCEADLEENIKKGKKCIRTPKISKPIKFELSGCTSMKTYRAKFCGVCTDGRCCTPHR 297

Qy   121 TTTLPVEFKCPDGEVMKKNMMFIKTCACHYNCPGDNDIFESLYYRKMYGDMA 172
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   298 TTTLPVEFKCPDGEVMKKNMMFIKTCACHYNCPGDNDIFESLYYRKMYGDMA 349
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RESULT 5

O97765 PIG
ID   O97765_PIG   PRELIMINARY;   PRT;   349 AA.
AC   O97765;
DT   01-MAY-1999 (TrEMBLrel. 10, Created)
DT   01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Connective tissue growth factor.
GN   Name=CTGF;
OS   Sus scrofa (Pig).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
OC   Sus.
OX   NCBI_TaxID=9823;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Uterus;
RA   Harding P.A., Brigstock D.R.;
RL   Submitted (SEP-1996) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; U70060; AAD00174.1; -; mRNA.
DR   GO; GO:0005576; C:extracellular region; IEA.
DR   GO; GO:0005520; F:insulin-like growth factor binding; IEA.
DR   GO; GO:0001558; P:regulation of cell growth; IEA.
DR   InterPro; IPR006208; Cys_knot.
DR   InterPro; IPR006207; Cys_knot_C.
DR   InterPro; IPR008867; Insl_gro_fac_pr.
DR   InterPro; IPR000884; TSP1.
DR   InterPro; IPR001007; VWF_C.
DR   Pfam; PF00007; Cys_knot; 1.
DR   Pfam; PF00219; IGFBP; 1.
DR   Pfam; PF00090; TSP_1; 1.
DR   Pfam; PF00093; VWC; 1.
DR   SMART; SM00041; CT; 1.
DR   SMART; SM00121; IB; 1.
DR   SMART; SM00209; TSP1; 1.
DR   SMART; SM00214; VWC; 1.
DR   PROSITE; PS01185; CTCK_1; 1.
DR   PROSITE; PS01225; CTCK_2; 1.
DR   PROSITE; PS00222; IGF_BINDING; 1.
DR   PROSITE; PS00092; TSP1; 1.
DR   PROSITE; PS01208; VWFC_1; 1.
DR   PROSITE; PS50184; VWFC_2; 1.
SQ   SEQUENCE 349 AA; 37946 MW; 35AB4275AC1D4B3A CRC64;

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Query Match    98.6%;    Score 943;    DB 2;    Length 349;
Best Local Similarity    97.7%;    Pred. No. 9.1e-80;
Matches    168;    Conservative    4;    Mismatches    0;    Indels    0;    Gaps    0;

Qy     1 ALAAYRLEDTFGPDPTMIRANCLVQTTEWSACSKTCGMGISTRVTNDNASCRLEKQSRLC 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   178 ALAAYRLEDTFGPDPTMRANCLVQTTEWSACSKTCGMGISTRVTNDNASCRLEKQSRLC 237

Qy    61 MVRPCEADLEENIKKGKKCIRTPKISKPIKFELSGCTSMKTYRAKFCGVCTDGRCCTPHR 120
          |||||||||||||||||||||||||||||||||||||:|||||||||||||||||||||
Db   238 MVRPCEADLEENIKKGKKCIRTPKISKPVKFELSGCTSVKTYRAKFCGVCTDGRCCTPHR 297

Qy   121 TTTLPVEFKCPDGEVMKKNMMFIKTCACHYNCPGDNDIFESLYYRKMYGDMA 172
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   298 TTTLPVEFKCPDGEVMKKSMMFIKTCACHYNCPGDNDIFESLYYRKMYGDMA 349
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RESULT 6
ID   CTGF_BOVIN   STANDARD;   PRT;   349 AA.
AC   O18739; Q9G171;
DT   15-JUL-1998 (Rel. 36, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   10-MAY-2005 (Rel. 47, Last annotation update)
DE   Connective tissue growth factor precursor.
GN   Name=CTGF; Synonyms=CCN2;
OS   Bos taurus (Bovine).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC   Pecora; Bovidae; Bovinae; Bos.

```
OX   NCBI_TaxID=9913;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Aorta;
RA   Lilienbaek B., Lin Z., Fotsis T., Schimanski M., Bierhaus A.,
RA   Kanitz M., Kauffmann G., Schweigerer L., Ziegler R., Nawroth P.P.;
RL   Submitted (AUG-1997) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Liver;
RA   Matabb M., Schwitters C., Hove M., Rupp S., Erondu N.E.;
RT   "Bovine connective tissue growth factor, organization of the
RT   chromosomal gene and demonstration of promoter activity.";
RL   Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: Major connective tissue growth factor secreted by
CC       vascular endothelial cells. Promotes proliferation and
CC       differentiation of chondrocytes (By similarity). Mediates heparin-
CC       and divalent cation-dependent cell adhesion in many cell types
CC       including fibroblasts, myofibroblasts, endothelial and epithelial
CC       cells (By similarity). Enhances fibroblast growth factor-induced
CC       DNA synthesis (By similarity).
CC   -!- SUBUNIT: Monomer (By similarity).
CC   -!- SUBCELLULAR LOCATION: Found in the extracellular matrix and as a
CC       soluble form (By similarity).
CC   -!- SIMILARITY: Belongs to the CCN family.
CC   -!- SIMILARITY: Contains 1 CTCK (C-terminal cystine knot-like) domain.
CC   -!- SIMILARITY: Contains 1 IGFBP domain.
CC   -!- SIMILARITY: Contains 1 TSP type-1 domain.
CC   -!- SIMILARITY: Contains 1 VWFC domain.
CC   --------------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   --------------------------------------------------------------------------
DR   EMBL; AF000137; AAB66596.1; -; mRNA.
DR   EMBL; AF309555; AAG30290.1; -; Genomic_DNA.
DR   InterPro; IPR006208; Cys_knot.
DR   InterPro; IPR006207; Cys_knot_C.
DR   InterPro; IPR012295; IGFBP_CNN.
DR   InterPro; IPR000867; IGFBP_like.
DR   InterPro; IPR000884; TSP1.
DR   InterPro; IPR001007; VWF_C.
DR   PIRSF; PIRSF036495; IGFBP_rP_CNN; 1.
DR   Pfam; PF00007; Cys_knot; 1.
DR   Pfam; PF00219; IGFBP; 1.
DR   Pfam; PF00090; TSP_1; 1.
DR   Pfam; PF00093; VWC; 1.
DR   SMART; SM00214; VWC; 1.
DR   PROSITE; PS01185; CTCK_1; 1.
DR   PROSITE; PS01225; CTCK_2; 1.
DR   PROSITE; PS00222; IGF_BINDING; 1.
DR   PROSITE; PS50092; TSP1; 1.
DR   PROSITE; PS01208; VWFC_1; 1.
DR   PROSITE; PS50184; VWFC_2; 1.
KW   Cell adhesion; DNA synthesis; Extracellular matrix; Heparin-binding;
KW   Signal.
FT   SIGNAL        1     26
FT   CHAIN        27    349       Connective tissue growth factor.
FT   DOMAIN       33    100       IGFBP.
FT   DOMAIN      101    167       VWFC.
FT   DOMAIN      198    243       TSP type-1.
FT   DOMAIN      256    330       CTCK.
FT   REGION      247    349       Heparin-binding (By similarity).
FT   DISULFID    256    293       By similarity.
FT   DISULFID    273    307       By similarity.
FT   DISULFID    287    325       By similarity.
FT   DISULFID    292    329       By similarity.
FT   CONFLICT     28     28       D -> DC (in Ref. 1).
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RESULT 7
CTGF_PIG
ID   CTGF_PIG      STANDARD;      PRT;    349 AA.
AC   O19113;
DT   15-JUL-1998 (Rel. 36, Created)
DT   15-JUL-1998 (Rel. 36, Last sequence update)
DT   10-MAY-2005 (Rel. 47, Last annotation update)
DE   Connective tissue growth factor precursor.
GN   Name=CTGF; Synonyms=CCN2;
OS   Sus scrofa (Pig).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
OC   Sus.
OX   NCBI_TaxID=9823;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Uterus;
RX   MEDLINE=97390475; PubMed=9227708; DOI=10.1074/jbc.272.32.20275;
RA   Brigstock D.R., Steffen C.L., Kim G.Y., Vegunta R.K., Diehl J.R.,
RA   Harding P.A.;
RT   "Purification and characterization of novel heparin-binding growth
RT   factors in uterine secretory fluids. Identification as heparin-
RT   regulated Mr 10,000 forms of connective tissue growth factor.";
RL   J. Biol. Chem. 272:20275-20282(1997).
CC   -!- FUNCTION: Major connective tissue growth factor secreted by
CC       vascular endothelial cells. Promotes proliferation and
CC       differentiation of chondrocytes (By similarity). Mediates heparin-
CC       and divalent cation-dependent cell adhesion in many cell types
CC       including fibroblasts, myofibroblasts, endothelial and epithelial
CC       cells (By similarity). Enhances fibroblast growth factor-induced
CC       DNA synthesis (By similarity).
CC   -!- SUBUNIT: Monomer (By similarity).
CC   -!- SUBCELLULAR LOCATION: Found in the extracellular matrix and as a
CC       soluble form (By similarity).
CC   -!- SIMILARITY: Belongs to the CCN family.
CC   -!- SIMILARITY: Contains 1 CTCK (C-terminal cystine knot-like) domain.
CC   -!- SIMILARITY: Contains 1 IGFBP domain.
CC   -!- SIMILARITY: Contains 1 TSP type-1 domain.
CC   -!- SIMILARITY: Contains 1 VWFC domain.
CC   --------------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   --------------------------------------------------------------------------
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Query Match            98.1%;   Score 938;  DB 1;  Length 349;
Best Local Similarity  98.3%;   Pred. No. 2.7e-79;
Matches 169;  Conservative 1;  Mismatches 2;  Indels 0;  Gaps 0;

Qy          1 ALAAYRLEDTFGPDPTMIRANCLVQTTEWSACSKTCGMGISTRVTNDNASCRLEKQSRLC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        178 ALAAYRPEDTFGPDPTMIRANCLVQTTEWSACSKTCGMGISTRVTNDNAPCRLEKQSRLC 237

Qy         61 MVRPCEADLEENIKKGKKCIRTPKISKPIKFELSGCTSMKTYRAKFCGVCTDGRCCTPHR 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        238 MVRPCEADLEENIKKGKKCIRTPKISKPIKFELSGCTSMKTYRAKFCGVCTDGRCCTPHR 297

Qy        121 TTTLPVEBFKCPDGEVMKKNMMFIKTCACHYNCPGGNDIFESLYYRKMYGDMA 172
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        298 TTTLPVEFKCPDGEVMKKSNMFIKTCACHYNCPGDNDIFESLYRKMYGDMA 349
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CC   -----------------------------------------------------------------------
DR   EMBL; U83916; AAC48756.1; -; mRNA.
DR   InterPro; IPR006208; Cys_knot.
DR   InterPro; IPR006207; Cys_knot_C.
DR   InterPro; IPR012395; IGFBP_CNN.
DR   InterPro; IPR000867; IGFBP_like.
DR   InterPro; IPR000884; TSP1.
DR   InterPro; IPR001007; VWF_C.
DR   Pfam; PF00007; Cys_knot; 1.
DR   Pfam; PF00219; IGFBP; 1.
DR   Pfam; PF00090; TSP_1; 1.
DR   Pfam; PF00093; VWC; 1.
DR   PIRSF; PIRSF036495; IGFBP_rP_CNN; 1.
DR   SMART; SM00041; CT; 1.
DR   SMART; SM00121; IB; 1.
DR   SMART; SM00209; TSP1; 1.
DR   SMART; SM00214; VWC; 1.
DR   PROSITE; PS01185; CTCK_1; 1.
DR   PROSITE; PS01225; CTCK_2; 1.
DR   PROSITE; PS00222; IGF_BINDING; 1.
DR   PROSITE; PS00092; TSP1; 1.
DR   PROSITE; PS01208; VWFC_1; 1.
DR   PROSITE; PS50184; VWFC_2; 1.
KW   Cell adhesion; DNA synthesis; Extracellular matrix; Heparin-binding;
KW   Signal.
FT   SIGNAL        1     26
FT   CHAIN        27    349       Connective tissue growth factor.
FT   DOMAIN       33    100       IGFBP.
FT   DOMAIN      101    167       VWFC.
FT   DOMAIN      198    243       TSP type-1.
FT   DOMAIN      256    330       CTCK.
FT   REGION      247    349       Heparin-binding (By similarity).
FT   DISULFID    256    293       By similarity.
FT   DISULFID    273    307       By similarity.
FT   DISULFID    284    323       By similarity.
FT   DISULFID    287    325       By similarity.
FT   DISULFID    292    329       By similarity.
SQ   SEQUENCE   349 AA;  38007 MW;  BB510E2B2B52D4A0 CRC64;

Query Match             98.0%;  Score 937;  DB 1;  Length 349;
Best Local Similarity   97.1%;
Matches  167;  Conservative    4;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 ALAAYRLEDTFGPDPTMIRANCLVQTTEWSACSKTCGMGISTRVTNDNASCRLEKQSRLC 60
            |||||||||||||||||:||||||||||||||||||||||||||||||:||||||||||
Db    178 ALAAYRLEDTFGPDPTMWRANCLVQTTEWSACSKTCGMGISTRVTNDNAFCRLEKQSRLC 237

Qy     61 MVRPCEADLEENIKKGKKCIRTPKISKPIKFELSGCTSMKTYRAKFCGVCTDGRCCTPHR 120
            |||||||||||||||||||||||||||||:|||||||||:|||||||||||||||||||
Db    238 MVRPCEADLEENIKKGKKCIRTPKISKPVKFELSGCTSVKTYRAKFCGVCTDGRCCTPHR 297

Qy    121 TTTLPVEFKCPDGEVMKSMMFIKTCACHYNCPGDNDIFESLYYRKMYGDMA 172
            ||||||||||||||||||||||||||||||||||||||||||||||||||
Db    298 TTTLPVEFKCPDGEVMKSMMFIKTCACHYNCPGDNDIFESLYYRKMYGDMA 349

RESULT 8

CTGF_RAT
ID   CTGF_RAT      STANDARD;      PRT;   347 AA.
AC   Q9R1E9; Q9WVS1;
DT   28-FEB-2003 (Rel. 41, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   10-MAY-2005 (Rel. 47, Last annotation update)
DE   Connective tissue growth factor precursor.
GN   Name=Ctgf; Synonyms=Ccn2;
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=20145935; PubMed=10679821;
RX   DOI=10.1002/(SICI)1097-4644(20000401)77:1<103::AID-JCB11>3.0.CO;2-G;
RA   Xu J., Smock S.L., Safadi F.F., Rosenzweig A.B., Odgren P.R.,
RA   Marks S.C. Jr., Owen T.A., Popoff S.N.;
RT   "Cloning the full-length cDNA for rat connective tissue growth factor:
RT   implications for skeletal development.";
RL   J. Cell. Biochem. 77:103-115(2000).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RA   Tezuka K., Tamatani T.;
RT   "Rattus norvegicus connective tissue growth factor.";
RL   Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.
-!-  FUNCTION: Major connective tissue growth factor secreted by
     vascular endothelial cells. Promotes proliferation and
     differentiation of chondrocytes (By similarity). Mediates heparin-
     and divalent cation-dependent cell adhesion in many cell types
     including fibroblasts, myofibroblasts, endothelial and epithelial
     cells (By similarity). Enhances fibroblast growth factor-induced
     DNA synthesis (By similarity).
-!-  SUBCELLULAR LOCATION: Secreted.
-!-  SIMILARITY: Belongs to the CCN family.
-!-  SIMILARITY: Contains 1 CTCK (C-terminal cystine knot-like) domain.
-!-  SIMILARITY: Contains 1 IGFBP domain.
-!-  SIMILARITY: Contains 1 TSP type-1 domain.
-!-  SIMILARITY: Contains 1 VWFC domain.
CC   -----------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   -----------------------------------------------------------------------
DR   EMBL; AF120275; AAD39132.1; -; mRNA.
DR   EMBL; AB023068; BAA82125.1; -; mRNA.
DR   Ensembl; ENSRNOG00000015036; Rattus norvegicus.
DR   InterPro; IPR006208; Cys_knot.
DR   InterPro; IPR006207; Cys_knot_C.
DR   InterPro; IPR012395; IGFBP_CNN.
DR   InterPro; IPR000867; IGFBP_like.
DR   InterPro; IPR000884; TSP1.
DR   InterPro; IPR001007; VWF_C.
DR   Pfam; PF00007; Cys_knot; 1.
DR   Pfam; PF00219; IGFBP; 1.
DR   Pfam; PF00090; TSP_1; 1.
DR   Pfam; PF00093; VWC; 1.
DR   PIRSF; PIRSF036495; IGFBP_rP_CNN; 1.
DR   SMART; SM00041; CT; 1.
DR   SMART; SM00121; IB; 1.
DR   SMART; SM00209; TSP1; 1.
DR   SMART; SM00214; VWC; 1.
DR   PROSITE; PS01185; CTCK_1; 1.
DR   PROSITE; PS01225; CTCK_2; 1.
DR   PROSITE; PS00222; IGF_BINDING; 1.
DR   PROSITE; PS00092; TSP1; 1.
DR   PROSITE; PS01208; VWFC_1; 1.
DR   PROSITE; PS50184; VWFC_2; 1.
KW   Cell adhesion; DNA synthesis; Extracellular matrix; Heparin-binding;
KW   Signal.
FT   SIGNAL        1     24
FT   CHAIN        25    347       Connective tissue growth factor.
FT   DOMAIN       31     98       IGFBP.
FT   DOMAIN       99    165       VWFC.
FT   DOMAIN      196    241       TSP type-1.
FT   DOMAIN      254    328       CTCK.
FT   REGION      245    347       Heparin-binding (By similarity).
FT   DISULFID    254    291       By similarity.
FT   DISULFID    271    305       By similarity.
FT   DISULFID    282    321       By similarity.
FT   DISULFID    285    323       By similarity.
FT   DISULFID    290    327       By similarity.
FT   CONFLICT     35     35       A -> R (in Ref. 2).
FT   CONFLICT     94     94       T -> P (in Ref. 2).
SQ   SEQUENCE   347 AA;  37756 MW;  CFBE1A19766B7B16 CRC64;
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Qy Query Match   97.7%; Score 934; DB 1; Length 347;
    Best Local Similarity 95.9%; Pred. No. 6.3e-79;
Matches 165; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

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Qy    1 ALAAYRLEDTFGPDPTMIRANCLVQTTEWSACSKTCGMGISTRVTNDNASCRLEKQSRLC  60
        ||||||||||||||||| |||||||||||||||||||||||||||||   ||||||||||
Db  176 ALAAYRLEDTFGPDPTMWRANCLVQTTEWSACSKTCGMGISTRVTNDNTFCRLEKQSRLC 235

Qy   61 MVRPCEADLEENIKKGKKCIRTPKISKPIKFELSGCTSMKTYRAKFCGVCTDGRCCTPHR 120
        ||||||||||||||||||||||||| :| :||||||||| :||||||||||||||||||||
Db  236 MVRPCEADLEENIKKGKKCIRTPKIAKPVKFELSGCTSVKTYRAKFCGVCTDGRCCTPHR 295

Qy  121 TTTLPVEFKCPDGEVMKKNMMFIKTCACHYNCPGDNDIFESLLYYRKMYGDMA 172
        |||||||||||||| ||||||||||||||||||||||||||| ||||||||||
Db  296 TTTLPVEFKCPDGEIMKKNMMFIKTCACHYNCPGDNDIFESLLYRKMYGDMA  347
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RESULT 9

ID   Q53YJ0_RAT   PRELIMINARY;   PRT;   347 AA.
AC   Q53YJ0;
DT   13-SEP-2005 (TrEMBLrel. 31, Created)
DT   13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT   13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE   Connective tissue growth related protein.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Ma L.N., Zou Y.L.;
RT   "Connective Tissue Growth Related Gene.";
RL   Submitted (APR-2004) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY596447; AAT08023.1; -; -.
SQ   SEQUENCE   347 AA; 37756 MW; CPBE1A19766B7B16 CRC64;

Query Match   97.7%; Score 934; DB 2; Length 347;
Best Local Similarity 95.9%; Pred. No. 6.3e-79;
Matches 165; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

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Qy    1 ALAAYRLEDTFGPDPTMIRANCLVQTTEWSACSKTCGMGISTRVTNDNASCRLEKQSRLC  60
        ||||||||||||||||| |||||||||||||||||||||||||||||   ||||||||||
Db  176 ALAAYRLEDTFGPDPTMWRANCLVQTTEWSACSKTCGMGISTRVTNDNTFCRLEKQSRLC 235

Qy   61 MVRPCEADLEENIKKGKKCIRTPKISKPIKFELSGCTSMKTYRAKFCGVCTDGRCCTPHR 120
        ||||||||||||||||||||||||| :| :||||||||| :||||||||||||||||||||
Db  236 MVRPCEADLEENIKKGKKCIRTPKIAKPVKFELSGCTSVKTYRAKFCGVCTDGRCCTPHR 295

Qy  121 TTTLPVEFKCPDGEVMKKNMMFIKTCACHYNCPGDNDIFESLLYYRKMYGDMA 172
        |||||||||||||| ||||||||||||||||||||||||||| ||||||||||
Db  296 TTTLPVEFKCPDGEIMKKNMMFIKTCACHYNCPGDNDIFESLLYRKMYGDMA  347
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RESULT 10

ID   CTGF_MOUSE   STANDARD;   PRT;   348 AA.
AC   P29268; Q922U0;
DT   01-DEC-1992 (Rel. 24, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   10-MAY-2005 (Rel. 47, Last annotation update)
DE   Connective tissue growth factor precursor (FISP-12 protein)
DE   (Hypertrophic chondrocyte-specific protein 24).
GN   Name=Ctgf; Synonyms=Ccn2, Fisp-12, Fisp12, Hcs24;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=91363290; PubMed=1888698;
RA   Ryseck R.-P., Macdonald-Bravo H., Mattei M.-G., Bravo R.;
RT   "Structure, mapping, and expression of fisp-12, a growth factor-
RT   inducible gene encoding a secreted cysteine-rich protein.";
RL   Cell Growth Differ. 2:225-233(1991).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=91229699; PubMed=2029337;
RA   Brunner A., Chinn J., Neubauer M.G., Purchio A.F.;
RT   "Identification of a gene family regulated by transforming growth
RT   factor-beta.";
RL   DNA Cell Biol. 10:293-300(1991).
RN   [3]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [4]
RP   FUNCTION, AND SUBCELLULAR LOCATION.
RX   MEDLINE=97327410; PubMed=9184077; DOI=10.1006/excr.1997.3548;
RA   Kireeva M.L., Latinkic B.V., Kolesnikova T.V., Chen C.-C., Yang G.P.,
RA   Abler A.S., Lau L.F.;
RT   "Cyr61 and Fisp12 are both ECM-associated signaling molecules:
RT   activities, metabolism, and localization during development.";
RL   Exp. Cell Res. 233:63-77(1997).
RN   [5]
RP   FUNCTION.
RX   MEDLINE=99182484; PubMed=10082563;
RA   Babic A.M., Chen C.-C., Lau L.F.;
RT   "Fisp12/mouse connective tissue growth factor mediates endothelial
RT   cell adhesion and migration through integrin alphavbeta3, promotes
RT   endothelial cell survival, and induces angiogenesis in vivo.";
RL   Mol. Cell. Biol. 19:2958-2966(1999).
CC   -!- FUNCTION: Major connective tissue mitoattractant secreted by
CC   vascular endothelial cells. Promotes proliferation and
CC   differentiation of chondrocytes (By similarity). Mediates heparin-
CC   and divalent cation-dependent cell adhesion in many cell types
CC   including fibroblasts, myofibroblasts, endothelial and epithelial
CC   cells (By similarity). Enhances fibroblast growth factor-induced
CC   DNA synthesis (By similarity).
CC   -!- SUBUNIT: Monomer (By similarity).
CC   -!- SUBCELLULAR LOCATION: Found in the extracellular matrix and as a
CC   soluble form.
CC   -!- TISSUE SPECIFICITY: Testis, spleen, kidney, lung, heart, and brain
CC   (lowest level in testis and highest in lung).
CC   -!- INDUCTION: By growth factors.
CC   -!- SIMILARITY: Belongs to the CCN family.
CC   -!- SIMILARITY: Contains 1 CTCK (C-terminal cystine knot-like) domain.
CC   -!- SIMILARITY: Contains 1 IGFBP domain.
CC   -!- SIMILARITY: Contains 1 TSP type-1 domain.
CC   -!- SIMILARITY: Contains 1 VWFC domain.
CC   ---
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its

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CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   -------------------------------------------------------------
DR   EMBL; M70641; AAA37627.1; -; Genomic_DNA.
DR   EMBL; M70642; AAA37628.1; -; mRNA.
DR   EMBL; M80263; AAA73135.1; -; mRNA.
DR   EMBL; BC006783; AAH06783.1; -; mRNA.
DR   PIR; A40578; A40578.
DR   Ensembl; ENSMUSG00000019997; Mus musculus.
DR   MGI; MGI:95537; Ctgf.
DR   GO; GO:0005578; C:extracellular matrix (sensu Metazoa); IDA.
DR   GO; GO:0005615; C:extracellular space; TAS.
DR   GO; GO:0008201; F:heparin binding; IDA.
DR   GO; GO:0005178; F:integrin binding; IDA.
DR   GO; GO:0001525; P:angiogenesis; IDA.
DR   GO; GO:0001502; P:cartilage condensation; IDA.
DR   GO; GO:0030154; P:cell differentiation; IDA.
DR   GO; GO:0016477; P:cell migration; IDA.
DR   GO; GO:0007160; P:cell-matrix adhesion; IDA.
DR   GO; GO:0008543; P:fibroblast growth factor receptor signaling . . .; IDA.
DR   GO; GO:0007229; P:integrin-mediated signaling pathway; IMP.
DR   GO; GO:0001503; P:ossification; IDA.
DR   InterPro; IPR006208; Cys_knot.
DR   InterPro; IPR006207; Cys_knot_C.
DR   InterPro; IPR012993; IGFBP_CNN.
DR   InterPro; IPR000867; IGFBP_like.
DR   InterPro; IPR000884; TSP1.
DR   PIRSF; PIRSF036495; IGFBP_rp_CNN; 1.
DR   InterPro; IPR001007; VWF_C.
DR   Pfam; PF00007; Cys_knot; 1.
DR   Pfam; PF00219; IGFBP; 1.
DR   Pfam; PF00090; TSP_1; 1.
DR   Pfam; PF00093; VWC; 1.
DR   SMART; SM00041; CT; 1.
DR   SMART; SM00121; IB; 1.
DR   SMART; SM00209; TSP1; 1.
DR   SMART; SM00214; VWC; 1.
DR   PROSITE; PS01208; VWFC_1; 1.
DR   PROSITE; PS50092; VWFC_2; 1.
DR   PROSITE; PS01225; CTCK_1; 1.
DR   PROSITE; PS50184; CTCK_2; 1.
KW   Signal.
KW   Cell adhesion; DNA synthesis; Extracellular matrix; Heparin-binding;
FT   SIGNAL        1     25
FT   CHAIN        26    348       Connective tissue growth factor.
FT   DOMAIN       32     99       IGFBP.
FT   DOMAIN      100    166       VWFC.
FT   DOMAIN      197    242       TSP type-1.
FT   DOMAIN      255    329       CTCK.
FT   REGION      246    348       Heparin-binding (By similarity).
FT   DISULFID    255    292       By similarity.
FT   DISULFID    272    306       By similarity.
FT   DISULFID    283    322       By similarity.
FT   DISULFID    286    324       By similarity.
FT   DISULFID    291    328       By similarity.
FT   CONFLICT    161    161       E -> K (in Ref. 1).
SQ   SEQUENCE   348 AA;  37794 MW;  4D7B6D9089174049 CRC64;

Qy   Query Match  97.7%;  Score 934;  DB 1;  Length 348;
     Best Local Similarity  95.9%;  Pred. No. 6.3e-79;
Matches 165;  Conservative 5;  Mismatches 2;  Indels 0;  Gaps 0;

Qy      1 ALAAYRLEDTFGPDPTMIRANCLVQTTEWSACSKTCGMGISTRVTNDNASCRLEKQSRLC 60
          ||||||||||||||||| |||||||||||||||||||||||||||||||||||||||||||
Db    177 ALAAYRLEDTFGPDPTMMRANCLVQTTEWSACSKTCGMGISTRVTNDNASCRLEKQSRLC 236

Qy     61 MVRPCEADLEENIKKGKKCIRTPKISKPIKFELSGCTSMKTYRAKFCGVCTDGRCCTPHR 120
          |||||||||||||||||||||||||||:||:|||||||:||||||||||||||||||||||
Db    237 MVRPCEADLEENIKKGKKCIRTPKIAKPVKFELSGCTSVKTYRAKFCGVCTDGRCCTPHR 296

Qy    121 TTTLPVEFKCPDGEVMKKNMMPIKTCACHYNCPGDNDIFESLYYRKMYGDMA 172
          |||| |||||||||:|||||||||||||||||||||||||||||||||||||
Db    297 TTTTLPVEFKCPDGEIMKKNMMPIKTCACHYNCPGDNDIFESLYYRKMYGDMA 348
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RESULT 11
Q98TQ8_CHICK
ID   Q98TQ8_CHICK   PRELIMINARY;      PRT;    344 AA.
AC   Q98TQ8;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE   Connective tissue growth factor precursor (Connective tissue growth
DE   factor/hypertrophic chondrocyte-specific protein 24).
OS   Gallus gallus (Chicken).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC   Gallus.
OX   NCBI_TaxID=9031;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=22559415; PubMed=12674494; DOI=10.1515/BC.2003.001;
RA   Mukudai Y., Kubota S., Takigawa M.;
RT   "Conserved repressive regulation of connective tissue growth
RT   factor/hypertrophic chondrocyte-specific gene 24 (ctgf/hcs24) enabled
RT   by different elements and factors among vertebrate species.";
RL   Biol. Chem. 384:1-9(2003).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=22984509; PubMed=14623326; DOI=10.1016/j.bbrc.2003.10.061;
RA   Gygi D., Zumstein P., Grossenbacher D., Altwegg L., Luscher T.F.,
RA   Gehring H.;
RT   "Human connective tissue growth factor expressed in Escherichia coli
RT   is a non-mitogenic inhibitor of apoptosis.";
RL   Biochem. Biophys. Res. Commun. 311:685-690(2003).
DR   EMBL; AF463517; AAL68834.1; -; mRNA.
DR   EMBL; AJ298335; CAC33438.1; -; mRNA.
DR   Ensembl; ENSGALG00000002909; Gallus gallus.
DR   GO; GO:0005576; C:extracellular region; IEA.
DR   GO; GO:0008083; F:growth factor activity; IEA.
DR   GO; GO:0005520; F:insulin-like growth factor binding; IEA.
DR   GO; GO:0001558; P:regulation of cell growth; IEA.
DR   InterPro; IPR006208; Cys_knot.
DR   InterPro; IPR006207; Cys_knot_C.
DR   InterPro; IPR000867; IGFBP.
DR   InterPro; IPR000884; TSP1.
DR   InterPro; IPR001007; VWF_C.
DR   Pfam; PF00007; Cys_knot; 1.
DR   Pfam; PF00219; IGFBP; 1.
DR   Pfam; PF00090; TSP_1; 1.
DR   Pfam; PF00093; VWC; 1.
DR   SMART; SM00041; CT; 1.
DR   SMART; SM00121; IB; 1.
DR   SMART; SM00209; TSP1; 1.
DR   SMART; SM00214; VWC; 1.
DR   PROSITE; PS01185; CTCK_1; 1.
DR   PROSITE; PS01225; CTCK_2; 1.
DR   PROSITE; PS00222; IGF_BINDING; 1.
DR   PROSITE; PS50092; TSP1; 1.
DR   PROSITE; PS01208; VWFC_1; 1.
DR   PROSITE; PS50184; VWFC_2; 1.
KW   Signal.
FT   SIGNAL        1     21       Potential.
FT   CHAIN        22    344       connective tissue growth factor.
SQ   SEQUENCE   344 AA;  37499 MW;  69E39AF69BF1D00 CRC64;

Qy   Query Match  96.8%;  Score 925;  DB 2;  Length 344;
     Best Local Similarity  95.3%;  Pred. No. 4.3e-78;
Matches 164;  Conservative 5;  Mismatches 3;  Indels 0;  Gaps 0;

Qy      1 ALAAYRLEDTFGPDPTMIRANCLVQTTEWSACSKTCGMGISTRVTNDNASCRLEKQSRLC 60
          |||||||||||||||||:|||||||||||||||||||||||||||||||:|||||||||||
Db    173 ALAAYRLEDTFGPDPTMMRANCLVQTTEWSACSKTCGMGISTRVTNDNAFCRLEKQSRLC 232
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Qy   61 MVRPCEADLEENIKKGKKCIRTPKISKPIKFELSGCTSMKTYRAKFCGVCTDGRCCTPHR 120
         ||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db  233 MVRPCEADLEENIKKGKKCIRTPKISKPIKFELSGCTSVKTYRAKFCGVCTDGRCCTPHR 292

Qy  121 TTTLPVEFKCPDGEVMKKNMMFIKTCACHYNCPGDNDIFESLYYRKMYGDMA 172
         ||||||||||||| | :|:|||||||||||||||||||||||||||||||
Db  293 TATLPVEFKCPDGEIMKKNMFIKTCACHYNCPGDNDIFESLYYRKMYGDMA 344
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RESULT 12
O42607_XENLA
ID   O42607_XENLA   PRELIMINARY;   PRT;   343 AA.
AC   O42607;
DT   01-JAN-1998 (TrEMBLrel. 05, Created)
DT   01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT   01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE   Connective tissue growth factor XCTGF.
OS   Xenopus laevis (African clawed frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OC   Xenopodinae; Xenopus; Xenopus.
OX   NCBI_TaxID=8355;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Ying Z., King M.L.;
RL   Submitted (DEC-1995) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; U43524; AAB67639.1; -; mRNA.
DR   EMBL; U43523; AAB67638.1; -; Genomic DNA.
DR   GO; GO:0005576; C:extracellular region; IEA.
DR   GO; GO:0008083; F:growth factor activity; IEA.
DR   GO; GO:0005520; F:insulin-like growth factor binding; IEA.
DR   GO; GO:0001558; P:regulation of cell growth; IEA.
DR   InterPro; IPR006208; Cys_knot.
DR   InterPro; IPR006207; Cys_knot_C.
DR   InterPro; IPR000867; Ins_gro_fac_pr.
DR   InterPro; IPR000884; TSP1.
DR   InterPro; IPR001007; VWF_C.
DR   Pfam; PF00007; Cys_knot; 1.
DR   Pfam; PF00219; IGFBP; 1.
DR   Pfam; PF00090; TSP_1; 1.
DR   Pfam; PF00093; VWC; 1.
DR   SMART; SM00041; CT; 1.
DR   SMART; SM00121; IB; 1.
DR   SMART; SM00209; TSP1; 1.
DR   SMART; SM00214; VWC; 1.
DR   PROSITE; PS01185; CTCK_1; 1.
DR   PROSITE; PS01225; CTCK_2; 1.
DR   PROSITE; PS50092; TSP1; 1.
DR   PROSITE; PS01208; VWFC_1; 1.
DR   PROSITE; PS50184; VWFC_2; 1.
SQ   SEQUENCE   343 AA; 37966 MW; 93F221C5DB565A81 CRC64;

Query Match   90.7%; Score 898; DB 2; Length 343;
Best Local Similarity   90.7%;
Matches 156; Conservative   11; Mismatches   5; Indels   0; Gaps   0;
                        Pred. No. 1.4e-75;

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Qy    1 ALAAYRLEDTFGPDPTMIRANCLVQTTEWSACSKTCGMGISTRVTNDNASCRLEKQSRLC 60
         || | |:|| :||||| ::||||||||||||||||||||||||||||||:|||||||||||
Db  172 ALPAFRMEETYGPDPSLIRANCLVQTTEWSACSKTCGMGISTRVTNDNEHCRLEKQSRLC 231

Qy   61 MVRPCEADLEENIKKGKKCIRTPKISKPIKFELSGCTSMKTYRAKFCGVCTDGRCCTPHR 120
         |||||||||||||||||||||||||||| ||| ||||| |||||||||||||||||||||
Db  232 MVRPCEADLEENIKKGKKCIRTPKISKPVKFEFSGCTSVKTYRAKFCGVCTDGRCCTPHR 291

Qy  121 TTTLPVEFKCPDGEVMKKNMMFIKTCACHYNCPGDNDIFESLYYRKMYGDMA 172
         ||||||||||||||||||| |||||||||:||||||||| ::| ||||||||
Db  292 TATLPVEFKCPDGEVMKKNMFIKTCACHFNCPGDNDIFEAMYRKMYGDMA 343
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RESULT 13
Q50SL5_XENLA
ID   Q50SL5_XENLA   PRELIMINARY;   PRT;   343 AA.
AC   Q50SL5;
DT   13-SEP-2005 (TrEMBLrel. 31, Created)
DT   13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT   13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
GN   Name=ctgf;
DE   Ctgf protein.
OS   Xenopus laevis (African clawed frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OC   Xenopodinae; Xenopus; Xenopus.
OX   NCBI_TaxID=8355;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Brain;
RX   MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA   Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA   Richardson P.;
RT   "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT   initiative.";
RL   Dev. Dyn. 225:384-391(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Brain;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [3]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Brain;
RA   Klein S., Gerhard D.S.;
RL   Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC094492; AAH94492.1; -; mRNA.
SQ   SEQUENCE   343 AA; 37879 MW; 8F448D73C7774FD0 CRC64;

Query Match   93.9%; Score 898; DB 2; Length 343;
Best Local Similarity   90.7%;
Matches 156; Conservative   11; Mismatches   5; Indels   0; Gaps   0;
                        Pred. No. 1.4e-75;

```
Qy    1 ALAAYRLEDTFGPDPTMIRANCLVQTTEWSACSKTCGMGISTRVTNDNASCRLEKQSRLC 60
         || | |:|| :||||| ::||||||||||||||||||||||||||||||:|||||||||||
Db  172 ALPAFRMEETYGPDPSLIRANCLVQTTEWSACSKTCGMGISTRVTNDNEHCRLEKQSRLC 231

Qy   61 MVRPCEADLEENIKKGKKCIRTPKISKPIKFELSGCTSMKTYRAKFCGVCTDGRCCTPHR 120
         |||||||||||||||||||||||||||| ||| ||||| |||||||||||||||||||||
Db  232 MVRPCEADLEENIKKGKKCIRTPKISKPVKFEFSGCTSVKTYRAKFCGVCTDGRCCTPHR 291

Qy  121 TTTLPVEFKCPDGEVMKKNMMFIKTCACHYNCPGDNDIFESLYYRKMYGDMA 172
         ||||||||||||||||||| |||||||||:||||||||| ::| ||||||||
Db  292 TATLPVEFKCPDGEVMKKNMFIKTCACHFNCPGDNDIFEAMYRKMYGDMA 343
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RESULT 14
Q5BKN7_XENTR
ID   Q5BKN7_XENTR   PRELIMINARY;   PRT;   343 AA.
AC   Q5BKN7;
DT   10-MAY-2005 (TrEMBLrel. 30, Created)

Left column

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Qy  121 TTTLPVEFKCPDGEVMKKKNMMFIKTCACHYNCPGDNDIFESLYYRKMYGDMA 172
        || |||||||||||::||||||||||||||||||||||||::||||||||||
Db  292 TATLPVEFKCPDGEIMKKKNMMFIKTCACHSNCPGDNDIFEAMYYRKMYGDMA 343
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DT   10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT   10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE   Connective tissue growth factor.
GN   Name=ctgf;
OS   Xenopus tropicalis (Western clawed frog) (Silurana tropicalis).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OC   Xenopodinae; Xenopus; Silurana.
OX   NCBI_TaxID=8364;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Whole body;
RX   MEDLINE=22382257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Feingold E.A., Grouse L.H., Derge J.G.,
RA   Strausberg R.L., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Klausner R.D., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Altschul S.F., Zeeberg B., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Hopkins R.F., Jordan H., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Diatchenko L., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Stapleton M., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P.,
RA   Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D.,
RA   Mullahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A.,
RA   Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M.,
RA   Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J.,
RA   Lu X., Gibbs R.A., Fahey J., Helton E., Ketteman M., Madan A.,
RA   Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C.,
RA   Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W.,
RA   Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J.,
RA   Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U.,
RA   Smailus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Whole body;
RL   Submitted (MAR-2005) to the EMBL/GenBank/DDBJ databases.
RA   Klein S., Gerhard D.S.;
DR   EMBL; BC091005; AAH91005.1; -; mRNA.
DR   InterPro; IPR006208; Cys_knot.
DR   InterPro; IPR006207; Cys_knot_C.
DR   InterPro; IPR012285; Fum_reductase_C.
DR   InterPro; IPR008867; Ins1_gro_fac_pr.
DR   InterPro; IPR000884; TSP1.
DR   InterPro; IPR001007; VWF_C.
DR   Pfam; PF00007; Cys_knot; 1.
DR   Pfam; PF00219; IGFBP; 1.
DR   Pfam; PF00090; TSP_1; 1.
DR   Pfam; PF00093; VWC; 1.
DR   SMART; SM00041; CT; 1.
DR   SMART; SM00121; IB; 1.
DR   SMART; SM00209; TSP1; 1.
DR   SMART; SM00214; VWC; 1.
DR   PROSITE; PS01185; CTCK_1; 1.
DR   PROSITE; PS01225; CTCK_2; 1.
DR   PROSITE; PS00222; IGF_BINDING; 1.
DR   PROSITE; PS50092; TSP1; 1.
DR   PROSITE; PS01208; VWFC_1; 1.
DR   PROSITE; PS50184; VWFC_2; 1.
SQ   SEQUENCE   343 AA; 37806 MW; EED6C9401F45AA5E CRC64;

Query Match   93.5%; Score 894; DB 2; Length 343;
Best Local Similarity   90.1%;
Matches 155; Conservative   12; Mismatches   5; Indels   0; Gaps   0;

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Db  172 ALPAFRMEETYGPDPSLIRANCLVQTTEWSACSKTCGMGISTRVTNDNEHCRLEKQSRLC 231

Qy   61 MVRPCEADLEENIKKGKKCIRTPKISKPIKFELSGCTSMKTYRAKFCGVCTDGRCCTPHR 120
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Db  232 MVRPCEADLEENIKKGKKCIRTPKISRPVKFELSGCTSVKTYRAKFCGVCTDGRCCTPHR 291
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Right column

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Qy  121 TTTLPVEFKCPDGEVMKKKNMMFIKTCACHYNCPGDNDIFESLYYRKMYGDMA 172
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Db  292 TATLPVEFKCPDGEIMKKKNMMFIKTCACHSNCPGDNDIFEAMYYRKMYGDMA 343
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RESULT 15
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AC   Q9PT80;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Connective tissue growth factor.
GN   Name=ctgf;
OS   Notophthalmus viridescens (Eastern newt) (Triturus viridescens).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Caudata; Salamandroidea; Salamandridae;
OC   Notophthalmus.
OX   NCBI_TaxID=8316;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Forelimb blastema;
RX   MEDLINE=99033008; PubMed=9811273; DOI=10.1016/S0378-1119(98)00478-8;
RA   Cash D.E., Gates P.B., Imokawa Y., Brockes J.P.;
RT   "Identification of newt connective tissue growth factor as a target of
RT   retinoid regulation in limb blastemal cells.";
RL   Gene 222:119-124(1998).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Forelimb blastema;
RA   Gates P.B.;
RL   Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AJ271167; CAB65965.1; -; mRNA.
DR   GO; GO:0005576; C:extracellular region; IEA.
DR   GO; GO:0008083; F:growth factor activity; IEA.
DR   GO; GO:0005520; F:insulin-like growth factor binding; IEA.
DR   GO; GO:0001558; P:regulation of cell growth; IEA.
DR   InterPro; IPR006208; Cys_knot.
DR   InterPro; IPR006207; Cys_knot_C.
DR   InterPro; IPR008867; Ins1_gro_fac_pr.
DR   InterPro; IPR000884; TSP1.
DR   InterPro; IPR001007; VWF_C.
DR   Pfam; PF00007; Cys_knot; 1.
DR   Pfam; PF00219; IGFBP; 1.
DR   Pfam; PF00093; VWC; 1.
DR   SMART; SM00041; CT; 1.
DR   SMART; SM00121; IB; 1.
DR   SMART; SM00209; TSP1; 1.
DR   SMART; SM00214; VWC; 1.
DR   PROSITE; PS01185; CTCK_1; 1.
DR   PROSITE; PS01225; CTCK_2; 1.
DR   PROSITE; PS00222; IGF_BINDING; 1.
DR   PROSITE; PS50092; TSP1; 1.
DR   PROSITE; PS01208; VWFC_1; 1.
DR   PROSITE; PS50184; VWFC_2; 1.
DR   PROSITE; PS00184; UNKNOWN_1.
SQ   SEQUENCE   347 AA; 38098 MW; 3B7E2399F27672C1 CRC64;

Query Match   93.4%; Score 893; DB 2; Length 347;
Best Local Similarity   91.3%;
Matches 157; Conservative   8; Mismatches   7; Indels   0; Gaps   0;

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Db  176 ALAVYRQEETVGPDSSLMRANCLVQTTEWSACSKTCGMGISTRVTNDNEMCRLEKQSRLC 235

Qy   61 MVRPCEADLEENIKKGKKCIRTPKISKPIKFELSGCTSMKTYRAKFCGVCTDGRCCTPHR 120
        ||||||||||||||||||||||||||||||||||||||:||||||||||||||||||||||
Db  236 MVRPCEADLEENIKKGKKCIRTPKISKPIKFELSGCTSVKTYRAKFCGVCTDGRCCTPHR 295
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OM protein - protein search, using sw model

Copyright (c) 1993 - 2006 Compugen Ltd.
GenCore version 5.1.6

Run on: January 9, 2006, 11:13:37 ; Search time 45 seconds
(without alignments)
316.005 Million cell updates/sec

Title: 956
Perfect score: 956
Sequence: 1 ALAAYRLEDTFGPDPTMIRA.........PGDNDIFESLYYRKMYGDMA 172

Scoring table: BLOSUM62
                Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database : Issued Patents AA:*
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2: /cgn2_6/ptodata/1/iaa/6_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/H_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	956	100.0	349	1	US-08-468-847B-14	Sequence 14, Appl
2	956	100.0	349	1	US-08-167-628-2	Sequence 2, Appl
3	956	100.0	349	1	US-08-386-680-2	Sequence 2, Appl
4	956	100.0	349	1	US-08-459-717-2	Sequence 2, Appl
5	956	100.0	349	1	US-08-712-302-2	Sequence 2, Appl
6	956	100.0	349	1	US-08-880-031-2	Sequence 2, Appli
7	956	100.0	349	1	US-09-054-368-2	Sequence 2, Appli
8	956	100.0	349	2	US-09-097-179-2	Sequence 2, Appli
9	956	100.0	349	2	US-09-054-274-2	Sequence 2, Appl
10	956	100.0	349	2	US-09-080-715-2	Sequence 2, Appl
11	956	100.0	349	2	US-09-056-704-2	Sequence 2, Appl
12	956	100.0	349	2	US-09-292-036-4	Sequence 4, Appl
13	956	100.0	349	26	US-09-253-316-26	Sequence 26, Appl
14	956	100.0	349	2	US-09-142-569-8	Sequence 8, Appl
15	956	100.0	349	2	US-09-495-448A-8	Sequence 8, Appl
16	956	100.0	349	2	US-09-461-688-2	Sequence 2, Appl
17	956	100.0	349	6141	US-09-949-016-6141	Sequence 6141, Ap
18	956	100.0	349	2	PCT-US96-08140-2	Sequence 2, Appl
19	956	100.0	349	4	US-09-582-337-2	Sequence 2, Appl
20	956	100.0	348	1	US-08-468-847B-15	Sequence 15, Appl
21	934	97.7	348	1	US-09-292-036-3	Sequence 3, Appl
22	934	97.7	348	2	US-09-142-569-6	Sequence 6, Appli
23	934	97.7	348	2	US-09-495-448A-6	Sequence 6, Appli
24	915	95.7	347	2	US-09-187-478-2	Sequence 2, Appli
25	915	95.7	347	2	US-09-292-036-2	Sequence 2, Appli
26	560	58.6	98	2	US-09-122-135-6	Sequence 6, Appl
27	546.5	57.2	351	1	US-08-468-847B-16	Sequence 16, Appl
28	546.5	57.2	351	2	US-09-495-448A-34	Sequence 34, Appl
29	519	54.3	357	1	US-08-468-847B-17	Sequence 17, Appl
30	519	54.3	357	2	US-09-253-316-25	Sequence 25, Appl
31	487.5	51.0	379	1	US-08-468-847B-11	Sequence 11, Appl
32	487.5	51.0	379	2	US-09-142-569-2	Sequence 2, Appli
33	487.5	51.0	379	2	US-09-495-448A-2	Sequence 2, Appli
34	485.5	50.8	381	2	US-09-348-815-2	Sequence 2, Appli
35	485.5	50.8	381	1	US-09-495-448A-13	Sequence 13, Appl
36	485.5	50.8	381	2	US-08-495-448A-4	Sequence 4, Appli
37	479.5	50.2	375	1	US-09-495-448A-13	Sequence 13, Appl
38	479.5	50.2	375	1	US-08-468-847B-13	Sequence 13, Appl
39	469.5	49.1	374	2	US-09-182-145-11	Sequence 11, Appl
40	468.5	49.0	375	1	US-08-459-101A-2	Sequence 2, Appli
41	423	44.2	367	2	US-09-182-145-12	Sequence 12, Appli
42	423	44.2	367	2	US-09-182-145-32	Sequence 32, Appl
43	405	42.4	339	2	US-09-182-145-33	Sequence 33, Appl
44	405	42.4	372	2	US-09-182-145-33	Sequence 33, Appl
45	404	42.3	339	2	US-09-182-145-36	Sequence 36, Appl

ALIGNMENTS

RESULT 1
US-08-468-847B-14
Sequence 14, Application US/08468847B
Patent No. 5780263
; GENERAL INFORMATION:
; APPLICANT: Hastings, Gregg A. and Adams, Mark D.
; TITLE OF INVENTION: Human CCN-Like Growth Factor
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
; ADDRESSEE: CECCHI, STEWART & OLSTEIN
; STREET: 6 BECKER FARM ROAD
; CITY: ROSELAND
; STATE: NEW JERSEY
; COUNTRY: USA
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 INCH DISKETTE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WORD PERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/468,847B
; FILING DATE: 6 June 1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: MULLINS, J.G.
; REGISTRATION NUMBER: 33,073
; REFERENCE/DOCKET NUMBER: 325800-442
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 348 AMINO ACIDS
; TYPE: AMINO ACID
; STRANDEDNESS:
; TOPOLOGY: LINEAR
; MOLECULE TYPE: PROTEIN
US-08-468-847B-14

Query Match   100.0%; Score 956; DB 1; Length 348;
Best Local Similarity 100.0%; Pred. No. 1.9e-83;
Matches 172; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 ALAAYRLEDTFGPDPTMIRANCLVQTTEWSACSKTCGMGLSTRVTNDNASCRLEKQSRLC 60
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Db   177 ALAAYRLEDTFGPDPTMIRANCLVQTTEWSACSKTCGMGISTRVTNDNASCRLEKQSRLC 236

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Db   237 MVRPCEADLEENIKKGKKCIRTPKISKPIKFELSGGCTSMKTYRAKFCGVCTDGRCCTPHR 296

Qy   121 TTTLPVEFKCPDGEVMKKNMMFIKTCACHYNCPGDNDIFESLYYRKMYGDMA 172
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RESULT 2
US-08-167-628-2
Sequence 2, Application US/08167628
; Patent No. 5408040
; GENERAL INFORMATION:
; APPLICANT: Grotendorst, Gary R.
; APPLICANT: Bradham Jr., Douglas M.,
; TITLE OF INVENTION: CONNECTIVE TISSUE GROWTH FACTOR
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Spensley Horn Jubas & Lubitz
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: US
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/167,628
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/752,427
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Wetherell, Jr., Ph.D., John W.
; REGISTRATION NUMBER: 31,678
; REFERENCE/DOCKET NUMBER: PD-1294
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-455-5100
; TELEFAX: 619-455-5110
INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 349 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-167-628-2

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Query Match             100.0%;   Score 956;  DB 1;   Length 349;
Best Local Similarity   100.0%;   Pred. No. 1.9e-83;
Matches   172;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy     1 ALAAYRLEDTFGPDPTMIRANCLVQTTEWSACSKTCGMGISTRVTNDNASCRLEKQSRLC 60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   178 ALAAYRLEDTFGPDPTMIRANCLVQTTEWSACSKTCGMGISTRVTNDNASCRLEKQSRLC 237

Qy    61 MVRPCEADLEENIKKGKKCIRTPKISKPIKFELSGGCTSMKTYRAKFCGVCTDGRCCTPHR 120
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Db   238 MVRPCEADLEENIKKGKKCIRTPKISKPIKFELSGGCTSMKTYRAKFCGVCTDGRCCTPHR 297

Qy   121 TTTLPVEFKCPDGEVMKKNMMFIKTCACHYNCPGDNDIFESLYYRKMYGDMA 172
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Db   298 TTTLPVEFKCPDGEVMKKNMMFIKTCACHYNCPGDNDIFESLYYRKMYGDMA 349
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RESULT 3
US-08-386-680-2
Sequence 2, Application US/08386680
; Patent No. 5585270
; GENERAL INFORMATION:
; APPLICANT: Grotendorst, Gary R.
; APPLICANT: Bradham Jr., Douglas M.,
; TITLE OF INVENTION: CONNECTIVE TISSUE GROWTH FACTOR
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Spensley Horn Jubas & Lubitz
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: US
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/386,680
; FILING DATE: 10-FEB-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/167,628
; FILING DATE:
; APPLICATION NUMBER: US/07/752,427
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Wetherell, Jr., Ph.D., John W.
; REGISTRATION NUMBER: 31,678
; REFERENCE/DOCKET NUMBER: PD-1294
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-455-5100
; TELEFAX: 619-455-5110
INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 349 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-386-680-2

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Query Match             100.0%;   Score 956;  DB 1;   Length 349;
Best Local Similarity   100.0%;   Pred. No. 1.9e-83;
Matches   172;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

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Db   178 ALAAYRLEDTFGPDPTMIRANCLVQTTEWSACSKTCGMGISTRVTNDNASCRLEKQSRLC 237

Qy    61 MVRPCEADLEENIKKGKKCIRTPKISKPIKFELSGGCTSMKTYRAKFCGVCTDGRCCTPHR 120
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Db   238 MVRPCEADLEENIKKGKKCIRTPKISKPIKFELSGGCTSMKTYRAKFCGVCTDGRCCTPHR 297

Qy   121 TTTLPVEFKCPDGEVMKKNMMFIKTCACHYNCPGDNDIFESLYYRKMYGDMA 172
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Db   298 TTTLPVEFKCPDGEVMKKNMMFIKTCACHYNCPGDNDIFESLYYRKMYGDMA 349
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RESULT 4
US-08-459-717-2
Sequence 2, Application US/08459717
; Patent No. 5770209
; GENERAL INFORMATION:
; APPLICANT: Grotendorst, Gary R.
; APPLICANT: Bradham Jr., Douglas M.,
; TITLE OF INVENTION: CONNECTIVE TISSUE GROWTH FACTOR
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Spensley Horn Jubas & Lubitz
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla

Left column

STATE: CA
COUNTRY: US
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US 07/752,427
FILING DATE: 02-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/752,427
FILING DATE: 30-AUG-1991
CLASSIFICATION: 536
APPLICATION NUMBER: US/08/459,717
FILING DATE:
CLASSIFICATION:
REGISTRATION NUMBER: 31,678
ATTORNEY/AGENT INFORMATION:
NAME: Wetherell, Jr., Ph.D., John W.
REFERENCE/DOCKET NUMBER: PD-1294
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-455-5100
TELEFAX: 619-455-5110
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 349 amino acid
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-459-717-2

Query Match   100.0%; Score 956; DB 1; Length 349;
Best Local Similarity 100.0%; Pred. No. 1.9e-83;
Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 178 ALAAYRLEDTFGPDPTMIRANCLVQTTEWSACSKTCGMGISTRVTNDNASCRLEKQSRLC 237

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Db 238 MVRPCEADLEENIKKGKKCIRTPKISKPIKFELSGCTSMKTYRAKFCGVCTDGRCCTPHR 297

Qy 121 TTTLPVEFKCPDGEVMKKNMMFIKTCACHYNCPGDNDIFESLYYRKMYGDMA 172
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Db 298 TTTLPVEFKCPDGEVMKKNMMFIKTCACHYNCPGDNDIFESLYYRKMYGDMA 349
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RESULT 5
US-08-712-302-2
; Sequence 2, Application US/08712302
; Patent No. 5783187
; GENERAL INFORMATION:
APPLICANT: Grotendorst, Gary R.
APPLICANT: Bradham Jr., Douglas M.,
TITLE OF INVENTION: CONNECTIVE TISSUE GROWTH FACTOR
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Spensley Horn Jubas & Lubitz
STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
STATE: CA
COUNTRY: US
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/712,302
FILING DATE: 11-SEP-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:

Right column

APPLICATION NUMBER: US 08/386,680
FILING DATE: 10-FEB-1995
APPLICATION NUMBER: US/08/167,628
FILING DATE:
APPLICATION NUMBER: US/07/752,427
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Wetherell, Jr., Ph.D., John W.
REGISTRATION NUMBER: 31,678
REFERENCE/DOCKET NUMBER: PD-1294
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-455-5100
TELEFAX: 619-455-5110
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 349 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-712-302-2

Query Match   100.0%; Score 956; DB 1; Length 349;
Best Local Similarity 100.0%; Pred. No. 1.9e-83;
Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 178 ALAAYRLEDTFGPDPTMIRANCLVQTTEWSACSKTCGMGISTRVTNDNASCRLEKQSRLC 237

Qy  61 MVRPCEADLEENIKKGKKCIRTPKISKPIKFELSGCTSMKTYRAKFCGVCTDGRCCTPHR 120
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Db 238 MVRPCEADLEENIKKGKKCIRTPKISKPIKFELSGCTSMKTYRAKFCGVCTDGRCCTPHR 297

Qy 121 TTTLPVEFKCPDGEVMKKNMMFIKTCACHYNCPGDNDIFESLYYRKMYGDMA 172
         |||||||||||||||||||||||||||||||||||||||||||||||||||
Db 298 TTTLPVEFKCPDGEVMKKNMMFIKTCACHYNCPGDNDIFESLYYRKMYGDMA 349
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RESULT 6
US-08-880-031-2
; Sequence 2, Application US/08880031
; Patent No. 5916756
; GENERAL INFORMATION:
APPLICANT: Grotendorst, Gary R.
APPLICANT: Bradham Jr., Douglas M.,
TITLE OF INVENTION: CONNECTIVE TISSUE GROWTH FACTOR
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Spensley Horn Jubas & Lubitz
STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
STATE: CA
COUNTRY: US
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/880,031
FILING DATE:
PRIOR APPLICATION DATA:
CLASSIFICATION:
APPLICATION NUMBER: US/08/167,628
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Wetherell, Jr., Ph.D., John W.
REGISTRATION NUMBER: 31,678
REFERENCE/DOCKET NUMBER: PD-1294
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-455-5100
TELEFAX: 619-455-5110

; INFORMATION FOR SEQ ID NO: 2:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 349 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
;   MOLECULE TYPE: protein
US-08-880-031-2

Qy Query Match   100.0%; Score 956; DB 1; Length 349;
Best Local Similarity 100.0%; Pred. No. 1.9e-83;
Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   1 ALAAYRLEDTFGPDPTMIRANCLVQTTEWSACSKTCGMGISTRVTNDNASCRLEKQSRLC 60
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Db   178 ALAAYRLEDTFGPDPTMIRANCLVQTTEWSACSKTCGMGISTRVTNDNASCRLEKQSRLC 237

Qy   61 MVRPCEADLEENIKKGKKCCIRTPKISKPIKFELSGCTSMKTYRAKFCGVCTDGRCCTPHR 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   238 MVRPCEADLEENIKKGKKCCIRTPKISKPIKFELSGCTSMKTYRAKFCGVCTDGRCCTPHR 297

Qy   121 TTTLPVEFKCPDGEVMKKNMMFIKTCACHYNCPGDNDIFESLYYRKMYGDMA 172
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   298 TTTLPVEFKCPDGEVMKKNMMFIKTCACHYNCPGDNDIFESLYYRKMYGDMA 349

RESULT 7
US-09-054-368-2
; Sequence 2, Application US/09054368
; Patent No. 6069006
;   GENERAL INFORMATION:
;   APPLICANT: University of South Florida
;   APPLICANT: Grotendorst, Gary R.
;   APPLICANT: Bradham, Jr., Douglass M.
;   TITLE OF INVENTION: CONNECTIVE TISSUE GROWTH FACTOR
;   FILE REFERENCE: 07414/003005
;   CURRENT APPLICATION NUMBER: US/09/054,368
;   CURRENT FILING DATE: 1998-04-02
;   EARLIER APPLICATION NUMBER: 08/386,680
;   EARLIER FILING DATE: 1995-02-10
;   EARLIER APPLICATION NUMBER: 08/459,717
;   EARLIER FILING DATE: 1995-06-02
;   EARLIER APPLICATION NUMBER: 08/167,628
;   EARLIER FILING DATE: 1993-12-14
;   NUMBER OF SEQ ID NOS: 9
;   SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
;   LENGTH: 349
;   TYPE: PRT
;   ORGANISM: Homo Sapiens
US-09-054-368-2

Qy Query Match   100.0%; Score 956; DB 2; Length 349;
Best Local Similarity 100.0%; Pred. No. 1.9e-83;
Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   178 ALAAYRLEDTFGPDPTMIRANCLVQTTEWSACSKTCGMGISTRVTNDNASCRLEKQSRLC 237

Qy   61 MVRPCEADLEENIKKGKKCCIRTPKISKPIKFELSGCTSMKTYRAKFCGVCTDGRCCTPHR 120
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Db   238 MVRPCEADLEENIKKGKKCCIRTPKISKPIKFELSGCTSMKTYRAKFCGVCTDGRCCTPHR 297

Qy   121 TTTLPVEFKCPDGEVMKKNMMFIKTCACHYNCPGDNDIFESLYYRKMYGDMA 172
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   298 TTTLPVEFKCPDGEVMKKNMMFIKTCACHYNCPGDNDIFESLYYRKMYGDMA 349

RESULT 8
US-09-097-179-2
; Sequence 2, Application US/09097179
; Patent No. 6149916
;   GENERAL INFORMATION:
;   APPLICANT: Grotendorst, Gary R.
;   APPLICANT: Bradham Jr., Douglas M.,
;   TITLE OF INVENTION: CONNECTIVE TISSUE GROWTH FACTOR
;   NUMBER OF SEQUENCES: 2
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Spensley Horn Jubas & Lubitz
;   STREET: 4225 Executive Square, Suite 1400
;   CITY: La Jolla
;   STATE: CA
;   COUNTRY: US
;   ZIP: 92037
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: Patentin Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/09/097,179
;   FILING DATE:
;   CLASSIFICATION:
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US 08/386,680
;   FILING DATE: 10-FEB-1995
;   APPLICATION NUMBER: US/08/167,628
;   FILING DATE:
;   APPLICATION NUMBER: US/07/752,427
;   FILING DATE:
;   ATTORNEY/AGENT INFORMATION:
;   NAME: Wetherell, Jr., Ph.D., John W.
;   REGISTRATION NUMBER: 31,678
;   REFERENCE/DOCKET NUMBER: PD-1294
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 619-455-5100
;   TELEFAX: 619-455-5110
; INFORMATION FOR SEQ ID NO: 2:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 349 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
;   MOLECULE TYPE: protein
US-09-097-179-2

Qy Query Match   100.0%; Score 956; DB 2; Length 349;
Best Local Similarity 100.0%; Pred. No. 1.9e-83;
Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   1 ALAAYRLEDTFGPDPTMIRANCLVQTTEWSACSKTCGMGISTRVTNDNASCRLEKQSRLC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   178 ALAAYRLEDTFGPDPTMIRANCLVQTTEWSACSKTCGMGISTRVTNDNASCRLEKQSRLC 237

Qy   61 MVRPCEADLEENIKKGKKCCIRTPKISKPIKFELSGCTSMKTYRAKFCGVCTDGRCCTPHR 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   238 MVRPCEADLEENIKKGKKCCIRTPKISKPIKFELSGCTSMKTYRAKFCGVCTDGRCCTPHR 297

Qy   121 TTTLPVEFKCPDGEVMKKNMMFIKTCACHYNCPGDNDIFESLYYRKMYGDMA 172
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   298 TTTLPVEFKCPDGEVMKKNMMFIKTCACHYNCPGDNDIFESLYYRKMYGDMA 349

RESULT 9
US-09-054-274-2
; Sequence 2, Application US/09054274
; Patent No. 6150101
;   GENERAL INFORMATION:
;   APPLICANT: University of South Florida
;   APPLICANT: Grotendorst, Gary R.
;   APPLICANT: Bradham, Jr., Douglas M.
;   TITLE OF INVENTION: METHODS OF IDENTIFYING A COMPOSITION
;   TITLE OF INVENTION: THAT ALTERS CONNECTIVE TISSUE GROWTH
;   TITLE OF INVENTION: FACTOR EXPRESSION (Amended)
;   FILE REFERENCE: 07414/003004
;   CURRENT APPLICATION NUMBER: US/09/054,274
;   CURRENT FILING DATE: 1998-04-02

; EARLIER APPLICATION NUMBER: 08/386,680
; EARLIER FILING DATE: 1995-02-10
; EARLIER APPLICATION NUMBER: 08/459,717
; EARLIER FILING DATE: 1995-06-02
; EARLIER APPLICATION NUMBER: 08/167,628
; EARLIER FILING DATE: 1993-12-14
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 349
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-054-274-2

Query Match   100.0%; Score 956; DB 2; Length 349;
Best Local Similarity   100.0%; Pred. No. 1.9e-83;
Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   1 ALAAYRLEDTFGPDPTMIRANCLVQTTEWSACSKTCGMGISTRVTNDNASCRLEKQSRLC 60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 178 ALAAYRLEDTFGPDPTMIRANCLVQTTEWSACSKTCGMGISTRVTNDNASCRLEKQSRLC 237

Qy   61 MVRPCEADLEENIKKGKKCIRTPKISKPIKFELSGCTSMKTYRAKFCGVCTDGRCCTPHR 120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 238 MVRPCEADLEENIKKGKKCIRTPKISKPIKFELSGCTSMKTYRAKFCGVCTDGRCCTPHR 297

Qy 121 TTTLPVEFKCPDGEVMKKNMMFIKTCACHYNCPGDNDIFESLYYRKMYGDMA 172
         |||||||||||||||||||||||||||||||||||||||||||||||||||
Db 298 TTTLPVEFKCPDGEVMKKNMMFIKTCACHYNCPGDNDIFESLYYRKMYGDMA 349

RESULT 10
US-09-080-715-2
Sequence 2, Application US/09080715
Patent No. 6190804
GENERAL INFORMATION:
APPLICANT: Grotendorst, Gary R.,
APPLICANT: Bradham Jr., Douglas M.,
TITLE OF INVENTION: CONNECTIVE TISSUE GROWTH FACTOR
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Spensley Horn Jubas & Lubitz
STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
STATE: CA
COUNTRY: US
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/080,715
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/167,628
FILING DATE:
APPLICATION NUMBER: US/07/752,427
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Wetherell, Jr. Ph.D., John W.
REGISTRATION NUMBER: 31,678
REFERENCE/DOCKET NUMBER: PD-1294
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-455-5100
TELEFAX: 619-455-5110
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 349 amino acids
TYPE: amino acid
TOPOLOGY: linear

; MOLECULE TYPE: protein
US-09-080-715-2

Query Match   100.0%; Score 956; DB 2; Length 349;
Best Local Similarity   100.0%; Pred. No. 1.9e-83;
Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   1 ALAAYRLEDTFGPDPTMIRANCLVQTTEWSACSKTCGMGISTRVTNDNASCRLEKQSRLC 60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 178 ALAAYRLEDTFGPDPTMIRANCLVQTTEWSACSKTCGMGISTRVTNDNASCRLEKQSRLC 237

Qy   61 MVRPCEADLEENIKKGKKCIRTPKISKPIKFELSGCTSMKTYRAKFCGVCTDGRCCTPHR 120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 238 MVRPCEADLEENIKKGKKCIRTPKISKPIKFELSGCTSMKTYRAKFCGVCTDGRCCTPHR 297

Qy 121 TTTLPVEFKCPDGEVMKKNMMFIKTCACHYNCPGDNDIFESLYYRKMYGDMA 172
         |||||||||||||||||||||||||||||||||||||||||||||||||||
Db 298 TTTLPVEFKCPDGEVMKKNMMFIKTCACHYNCPGDNDIFESLYYRKMYGDMA 349

RESULT 11
US-09-056-704-2
Sequence 2, Application US/09056704
Patent No. 6232064
GENERAL INFORMATION:
APPLICANT: Grotendorst, Gary R.
APPLICANT: Bradham, Jr., Douglas M.
TITLE OF INVENTION: DISORDER ASSOCIATED WITH CONNECTIVE
TITLE OF INVENTION: TISSUE GROWTH FACTOR (Amended)
TITLE OF INVENTION: CHARACTERIZED BY A CELL PROLIFERATIVE
TITLE OF INVENTION: METHODS OF DIAGNOSING A PATHOLOGY
FILE REFERENCE: 07414/003002
CURRENT APPLICATION NUMBER: US/09/056,704
CURRENT FILING DATE: 1998-03-03
EARLIER APPLICATION NUMBER: 08/386,680
EARLIER FILING DATE: 1995-02-10
EARLIER APPLICATION NUMBER: 08/459,717
EARLIER FILING DATE: 1995-06-02
EARLIER APPLICATION NUMBER: 08/167,628
EARLIER FILING DATE: 1993-12-14
NUMBER OF SEQ ID NOS: 9
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 349
TYPE: PRT
ORGANISM: Homo Sapiens
US-09-056-704-2

Query Match   100.0%; Score 956; DB 2; Length 349;
Best Local Similarity   100.0%; Pred. No. 1.9e-83;
Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   1 ALAAYRLEDTFGPDPTMIRANCLVQTTEWSACSKTCGMGISTRVTNDNASCRLEKQSRLC 60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 178 ALAAYRLEDTFGPDPTMIRANCLVQTTEWSACSKTCGMGISTRVTNDNASCRLEKQSRLC 237

Qy   61 MVRPCEADLEENIKKGKKCIRTPKISKPIKFELSGCTSMKTYRAKFCGVCTDGRCCTPHR 120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 238 MVRPCEADLEENIKKGKKCIRTPKISKPIKFELSGCTSMKTYRAKFCGVCTDGRCCTPHR 297

Qy 121 TTTLPVEFKCPDGEVMKKNMMFIKTCACHYNCPGDNDIFESLYYRKMYGDMA 172
         |||||||||||||||||||||||||||||||||||||||||||||||||||
Db 298 TTTLPVEFKCPDGEVMKKNMMFIKTCACHYNCPGDNDIFESLYYRKMYGDMA 349

RESULT 12
US-09-292-036-4
Sequence 4, Application US/09292036
Patent No. 6358741
GENERAL INFORMATION:
APPLICANT: FIBROGEN, INC
APPLICANT: SCHMIDT, Brian

```
APPLICANT: ALLEN, Margaret
APPLICANT: SVERDRUP
APPLICANT: CARMICHAEL, David, Fran
TITLE OF INVENTION: CONNECTIVE TISSUE GROWTH FACTOR (CTGF) AND METHODS OF USE
FILE REFERENCE: FIBRO1100-1
CURRENT APPLICATION NUMBER: US/09/292,036
CURRENT FILING DATE: 1999-04-14
PRIOR APPLICATION NUMBER: US 09/292,036
PRIOR FILING DATE: 1999-04-14
PRIOR APPLICATION NUMBER: US 09/187,478
PRIOR FILING DATE: 1998-11-06
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PatentIn version 3.0
SEQ ID NO 4
  LENGTH: 349
  TYPE: PRT
  ORGANISM: Human
US-09-292-036-4
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RESULT 13
US-09-253-316-26
Sequence 26, Application US/0925336
Patent No. 6395890
GENERAL INFORMATION:
APPLICANT: Sheppard, Paul O.
APPLICANT: Jaspers, Stephen R.
TITLE OF INVENTION: CONNECTIVE TISSUE GROWTH FACTOR HOMOLOGS
FILE REFERENCE: 97-75
CURRENT APPLICATION NUMBER: US/09/253,316
CURRENT FILING DATE: 1999-02-19
EARLIER APPLICATION NUMBER: US 60/075,300
EARLIER FILING DATE: 1998-02-20
NUMBER OF SEQ ID NOS: 34
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 26
  LENGTH: 349
  TYPE: PRT
  ORGANISM: Homo sapiens
US-09-253-316-26

Query Match        100.0%;   Score 956;  DB 2;   Length 349;
Best Local Similarity   100.0%;   Pred. No. 1.9e-83;
Matches 172;  Conservative   0;  Mismatches   0;   Indels   0;   Gaps   0;

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        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  178 ALAAYRLEDTFGPDPTMIRANCLVQTTEWSACSKTCGMGISTRVTNDNASCRLEKQSRLC 237

Qy   61 MVRPCEADLEENIKKGKKCIRTPKISKPIKFELSGCTSMKTYRAKFCGVCTDGRCCTPHR 120
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Db  238 MVRPCEADLEENIKKGKKCIRTPKISKPIKFELSGCTSMKTYRAKFCGVCTDGRCCTPHR 297

Qy  121 TTTLPVEFKCPDGEVMKKNMMFIKTCACHYNCPGDNDIFESLYYRKMYGDMA 172
        |||||||||||||||||||||||||||||||||||||||||||||||||||
Db  298 TTTLPVEFKCPDGEVMKKNMMFIKTCACHYNCPGDNDIFESLYYRKMYGDMA 349
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RESULT 14
US-09-142-569-8
Sequence 8, Application US/09142569
Patent No. 6413735
GENERAL INFORMATION:
APPLICANT: Lau, Lester F.
TITLE OF INVENTION: Extracellular Matrix Signalling Molecules
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
  ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
  STREET: 6300 Sears Tower, 233 South Wacker Drive
  CITY: Chicago
  STATE: Illinois
  COUNTRY: United States of America
  ZIP: 60606-6402
COMPUTER READABLE FORM:
  MEDIUM TYPE: Floppy disk
  COMPUTER: IBM PC compatible
  OPERATING SYSTEM: PC-DOS/MS-DOS
  SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
  APPLICATION NUMBER: US/09/142,569
  FILING DATE: 02-Apr-1999
  CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
  NAME: Clough, David W.
  REGISTRATION NUMBER: 36,107
  REFERENCE/DOCKET NUMBER: 28758/33766
TELECOMMUNICATION INFORMATION:
  TELEPHONE: 312/474-6300
  TELEFAX: 312/474-0448
  TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
  LENGTH: 349 amino acids
  TYPE: amino acid
  STRANDEDNESS: single
  TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
  NAME/KEY: misc_feature
  OTHER INFORMATION: "CTGF amino acid sequence"
SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-09-142-569-8

Query Match        100.0%;   Score 956;  DB 2;   Length 349;
Best Local Similarity   100.0%;   Pred. No. 1.9e-83;
Matches 172;  Conservative   0;  Mismatches   0;   Indels   0;   Gaps   0;

Qy    1 ALAAYRLEDTFGPDPTMIRANCLVQTTEWSACSKTCGMGISTRVTNDNASCRLEKQSRLC 60
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  178 ALAAYRLEDTFGPDPTMIRANCLVQTTEWSACSKTCGMGISTRVTNDNASCRLEKQSRLC 237

Qy   61 MVRPCEADLEENIKKGKKCIRTPKISKPIKFELSGCTSMKTYRAKFCGVCTDGRCCTPHR 120
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  238 MVRPCEADLEENIKKGKKCIRTPKISKPIKFELSGCTSMKTYRAKFCGVCTDGRCCTPHR 297

Qy  121 TTTLPVEFKCPDGEVMKKNMMFIKTCACHYNCPGDNDIFESLYYRKMYGDMA 172
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Db  298 TTTLPVEFKCPDGEVMKKNMMFIKTCACHYNCPGDNDIFESLYYRKMYGDMA 349
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RESULT 15
US-09-461-688-2
Sequence 2, Application US/09461688
Patent No. 6492129
GENERAL INFORMATION:
APPLICANT: Grotendorst, Gary R.
TITLE OF INVENTION: CONNECTIVE TISSUE GROWTH FACTOR
TITLE OF INVENTION: FRAGMENTS AND METHODS AND USES THEREOF
FILE REFERENCE: FIBRO1140-2
CURRENT APPLICATION NUMBER: US/09/461,688
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; CURRENT FILING DATE: 1999-12-14
; PRIOR APPLICATION NUMBER:  60/112,240
; PRIOR FILING DATE:  1998-12-14
; PRIOR APPLICATION NUMBER:  60/112,241
; PRIOR FILING DATE:  1998-12-14
; NUMBER OF SEQ ID NOS:  4
; SOFTWARE:  FastSEQ for Windows Version 4.0
;
; SEQ ID NO 2
; LENGTH: 349
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-461-688-2

Query Match             100.0%;  Score 956;  DB 2;  Length 349;
Best Local Similarity   100.0%;  Pred. No. 1.9e-83;
Matches 172;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy      1 ALAAYRLEDTFGPDPTMIRANCLVQTTEWSACSKTCGMGISTRVTNDDNASCRLEKQSRLC 60
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Db    178 ALAAYRLEDTFGPDPTMIRANCLVQTTEWSACSKTCGMGISTRVTNDDNASCRLEKQSRLC 237

Qy     61 MVRPCEADLEENIKKGKKCIRTPKISKPIKFELSGCTSMKTYRAKFCGVCTDGRCCTPHR 120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    238 MVRPCEADLEENIKKGKKCIRTPKISKPIKFELSGCTSMKTYRAKFCGVCTDGRCCTPHR 297

Qy    121 TTTLPVEFKCPDGEVMKQNMMFIKTCACHYNCPGDNDIFESLYYRKMYGDMA 172
            ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    298 TTTLPVEFKCPDGEVMKQNMMFIKTCACHYNCPGDNDIFESLYYRKMYGDMA 349
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Job time : 46 secs

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OM protein - protein search, using sw model

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GenCore version 5.1.6

Run on: January 9, 2006, 11:19:18 ; Search time 115 seconds
                                               (without alignment)
                                               624.927 Million cell updates/sec

Title: US-09-461-646-4
Perfect score: 956
Sequence: 1 ALAAYRLEDTFGPDPTMIRA............PGDNDIFESLYYRKMYGDMA 172

Scoring table:
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              Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Published Applications AA Main:*
              1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
              2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
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              5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
              6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	956	100.0	172	4	US-10-658-856-4	Sequence 4, Appli
2	956	100.0	348	4	US-09-853-625B-14	Sequence 14, Appli
3	956	100.0	349	4	US-10-101-040-4	Sequence 4, Appli
4	956	100.0	349	4	US-10-011-859-26	Sequence 26, Appli
5	956	100.0	349	4	US-10-053-753-8	Sequence 8, Appli
6	956	100.0	349	4	US-10-060-036-173	Sequence 173, App
7	956	100.0	349	4	US-10-171-311-46	Sequence 46, Appl
8	956	100.0	349	4	US-10-205-823-78	Sequence 78, Appl
9	956	100.0	349	4	US-10-245-977-2	Sequence 2, Appli
10	956	100.0	349	4	US-10-315-568-2	Sequence 2, Appli
11	956	100.0	349	4	US-10-394-015-4	Sequence 4, Appli
12	956	100.0	349	4	US-10-131-985-7	Sequence 7, Appli
13	956	100.0	349	4	US-10-182-432-8	Sequence 8, Appli
14	956	100.0	349	4	US-10-338-587A-2	Sequence 2, Appli
15	956	100.0	349	4	US-10-428-487-44	Sequence 44, Appl
16	956	100.0	349	4	US-10-464-368-55	Sequence 55, Appl
17	956	100.0	349	4	US-10-658-856-2	Sequence 2, Appli
18	956	100.0	349	4	US-10-627-604-14	Sequence 14, Appl
19	956	100.0	349	4	US-10-721-336-3	Sequence 3, Appli
20	956	100.0	349	4	US-10-755-889-60	Sequence 60, Appl
21	956	100.0	349	4	US-10-858-186-2	Sequence 2, Appli
22	956	100.0	349	5	US-10-902-895-8	Sequence 8, Appl
23	956	100.0	349	5	US-10-901-417-7	Sequence 7, Appl
24	956	100.0	349	5	US-10-627-604-14	Sequence 14, Appl
25	956	100.0	349	6	US-11-955-860A-1	Sequence 1, Appli
26	956	100.0	349	6	US-11-051-454-78	Sequence 78, Appl
27	956	100.0	349	6	US-11-149-564-26	Sequence 26, Appl
28	938	98.1	226	5	US-10-617-316-132	Sequence 132, App
29	938	98.1	226	5	US-10-617-316-163	Sequence 163, App
30	938	98.1	349	4	US-10-245-977-5	Sequence 5, Appli
31	937	98.0	349	4	US-10-245-977-6	Sequence 6, Appli
32	934	97.7	347	4	US-10-390-986-2	Sequence 2, Appli
33	934	97.7	347	4	US-10-464-368-56	Sequence 56, Appl
34	934	97.7	347	4	US-09-853-625B-15	Sequence 15, Appl
35	934	97.7	348	4	US-10-101-040-3	Sequence 3, Appli
36	934	97.7	348	4	US-10-053-753-6	Sequence 6, Appli
37	934	97.7	348	4	US-10-182-432-6	Sequence 6, Appli
38	934	97.7	348	4	US-10-245-977-8	Sequence 8, Appli
39	934	97.7	348	4	US-10-464-368-54	Sequence 54, Appl
40	934	97.7	348	4	US-10-627-604-15	Sequence 15, Appl
41	934	97.7	348	4	US-10-902-895-6	Sequence 6, Appl
42	934	97.7	348	4	US-10-627-604-15	Sequence 15, Appl
43	934	97.7	348	5	US-10-080-173-2	Sequence 2, Appli
44	915	95.7	347	4	US-10-080-173-2	Sequence 2, Appli
45	915	95.7	347	4	US-10-101-040-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-10-658-856-4

; Sequence 4, Application US/10658856
; Publication No. US20040092450A1
; GENERAL INFORMATION:
; APPLICANT: Fibrogen, Inc.
; APPLICANT: Groetendorst, Gary
; APPLICANT: Neff, Thomas
; TITLE OF INVENTION: Connective Tissue Growth Factor Fragments and Methods and Uses Ti
; FILE REFERENCE: FIBRO1130-2
; CURRENT APPLICATION NUMBER: US/10/658,856
; CURRENT FILING DATE: 2003-09-09
; PRIOR APPLICATION NUMBER: US/09/461,646
; PRIOR FILING DATE: 1999-12-14
; PRIOR APPLICATION NUMBER: 60/112,240
; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: 60/112,241
; PRIOR FILING DATE: 1998-12-14
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 172
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-658-856-4

Query Match   100.0%; Score 956; DB 4; Length 172;
Best Local Similarity   100.0%; Pred. No. 8.4e-84;
Matches 172; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 ALAAYRLEDTFGPDPTMIRANCLVQTTEWSACSKTCGMGISTRVTNDNASCRLEKQSRLC 60
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Db   1 ALAAYRLEDTFGPDPTMIRANCLVQTTEWSACSKTCGMGISTRVTNDNASCRLEKQSRLC 60

Qy   61 MVRPCEADLEENIKKGKKCIRTPKISKPIKFELSGCTSMKTYRAKFCGVCTDGRCCTPHR 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 MVRPCEADLEENIKKGKKCIRTPKISKPIKFELSGCTSMKTYRAKFCGVCTDGRCCTPHR 120

Qy   121 TTTLPVEFKCPDGEVMKKNMMFIKTCACHYNCPGDNDIFESLYYRKMYGDMA 172
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 TTTLPVEFKCPDGEVMKKNMMFIKTCACHYNCPGDNDIFESLYYRKMYGDMA 172

RESULT 2
US-09-853-625B-14

; Sequence 14, Application US/09853625B
; Patent No. US20020049304A1
; GENERAL INFORMATION:
; APPLICANT: Hastings, Gregg A. and Adams, Mark D.
; TITLE OF INVENTION: Human CCN-Like Growth Factor
;

NUMBER OF SEQUENCES: 20
          CORRESPONDENCE ADDRESS:
               ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
                    CECCHI, STEWART & OLSTEIN
               STREET: 6 BECKER FARM ROAD
               CITY: ROSELAND
               STATE: NEW JERSEY
               COUNTRY: USA
               ZIP: 07068
          COMPUTER READABLE FORM:
               MEDIUM TYPE: 3.5 INCH DISKETTE
               COMPUTER: IBM PS/2
               OPERATING SYSTEM: MS-DOS
               SOFTWARE: WORD PERFECT 5.1
          CURRENT APPLICATION DATA:
               APPLICATION NUMBER: US/09/853,625B
               FILING DATE: 14-May-2001
               CLASSIFICATION: <Unknown>
          PRIOR APPLICATION DATA:
               APPLICATION NUMBER: 09/053,587
               FILING DATE: <Unknown>
          ATTORNEY/AGENT INFORMATION:
               NAME: MULLINS, J.G.
               REGISTRATION NUMBER: 33,073
               REFERENCE/DOCKET NUMBER: 325800-442
          TELECOMMUNICATION INFORMATION:
               TELEPHONE: 201-994-1700
               TELEFAX: 201-994-1744
     INFORMATION FOR SEQ ID NO: 14:
          SEQUENCE CHARACTERISTICS:
               LENGTH: 348 AMINO ACIDS
               TYPE: AMINO ACID
               STRANDEDNESS: <Unknown>
               TOPOLOGY: LINEAR
          MOLECULE TYPE: PROTEIN
          SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-09-853-625B-14

Query Match   100.0%; Score 956; DB 3; Length 348;
Best Local Similarity   100.0%; Pred. No. 1.8e-83;
Matches 172; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 ALAAYRLEDTFGPDPTMIRANCLVQTTEWSACSKTCGMGISTRVTNDNASCRLEKQSRLC 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   177 ALAAYRLEDTFGPDPTMIRANCLVQTTEWSACSKTCGMGISTRVTNDNASCRLEKQSRLC 236

Qy   61 MVRPCEADLEENIKKGKKCIRTPKISKPIKFELSGCTSMKTYRAKFCGVCTDGRCCTPHR 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   237 MVRPCEADLEENIKKGKKCIRTPKISKPIKFELSGCTSMKTYRAKFCGVCTDGRCCTPHR 296

Qy   121 TTTLPVEFKCPDGEVMKKNMMFIKTCACHYNCPGDNDIFESLYYRKMYGDMA 172
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   297 TTTLPVEFKCPDGEVMKKNMMFIKTCACHYNCPGDNDIFESLYYRKMYGDMA 348

RESULT 3
US-10-101-040-4
; Sequence 4, Application US/10101040
; Publication No. US20020142353A1
; GENERAL INFORMATION:
; APPLICANT: FIBROGEN, INC
; APPLICANT: SCHMIDT, Brian
; APPLICANT: ALLEN, Margaret
; APPLICANT: SVERDRUP, Fran
; APPLICANT: CARMICHAEL, David
; TITLE OF INVENTION: CONNECTIVE TISSUE GROWTH FACTOR (CTGF) AND METHODS OF
; TITLE OF INVENTION: USE
; FILE REFERENCE: FIBRO1100-1
; CURRENT APPLICATION NUMBER: US/10/101,040
; CURRENT FILING DATE: 2002-03-18
; PRIOR APPLICATION NUMBER: 09/292,036
; PRIOR FILING DATE: 1999-04-14
; PRIOR APPLICATION NUMBER: US 09/292,036

; PRIOR FILING DATE: 1999-04-14
; PRIOR APPLICATION NUMBER: US 09/187,478
; PRIOR FILING DATE: 1998-11-06
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 4
; LENGTH: 349
; TYPE: PRT
; ORGANISM: Human
US-10-101-040-4

Query Match   100.0%; Score 956; DB 4; Length 349;
Best Local Similarity   100.0%; Pred. No. 1.8e-83;
Matches 172; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 ALAAYRLEDTFGPDPTMIRANCLVQTTEWSACSKTCGMGISTRVTNDNASCRLEKQSRLC 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   178 ALAAYRLEDTFGPDPTMIRANCLVQTTEWSACSKTCGMGISTRVTNDNASCRLEKQSRLC 237

Qy   61 MVRPCEADLEENIKKGKKCIRTPKISKPIKFELSGCTSMKTYRAKFCGVCTDGRCCTPHR 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   238 MVRPCEADLEENIKKGKKCIRTPKISKPIKFELSGCTSMKTYRAKFCGVCTDGRCCTPHR 297

Qy   121 TTTLPVEFKCPDGEVMKKNMMFIKTCACHYNCPGDNDIFESLYYRKMYGDMA 172
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   298 TTTLPVEFKCPDGEVMKKNMMFIKTCACHYNCPGDNDIFESLYYRKMYGDMA 349

RESULT 4
US-10-011-859-26
; Sequence 26, Application US/10011859
; Publication No. US20020147328A1
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Jaspers, Stephen R.
; TITLE OF INVENTION: CONNECTIVE TISSUE GROWTH FACTOR HOMOLOGS
; FILE REFERENCE: 97-75
; CURRENT APPLICATION NUMBER: US/10/011,859
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/253,316
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-02-19
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/075,300
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-02-20
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 26
; LENGTH: 349
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-011-859-26

Query Match   100.0%; Score 956; DB 4; Length 349;
Best Local Similarity   100.0%; Pred. No. 1.8e-83;
Matches 172; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 ALAAYRLEDTFGPDPTMIRANCLVQTTEWSACSKTCGMGISTRVTNDNASCRLEKQSRLC 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   178 ALAAYRLEDTFGPDPTMIRANCLVQTTEWSACSKTCGMGISTRVTNDNASCRLEKQSRLC 237

Qy   61 MVRPCEADLEENIKKGKKCIRTPKISKPIKFELSGCTSMKTYRAKFCGVCTDGRCCTPHR 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   238 MVRPCEADLEENIKKGKKCIRTPKISKPIKFELSGCTSMKTYRAKFCGVCTDGRCCTPHR 297

Qy   121 TTTLPVEFKCPDGEVMKKNMMFIKTCACHYNCPGDNDIFESLYYRKMYGDMA 172
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   298 TTTLPVEFKCPDGEVMKKNMMFIKTCACHYNCPGDNDIFESLYYRKMYGDMA 349

RESULT 5
US-10-053-753-8
; Sequence 8, Application US/10053753
; Publication No. US20020150986A1
; GENERAL INFORMATION:

APPLICANT: Lau, Lester F.
TITLE OF INVENTION: Extracellular Matrix Signalling Molecules
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/053,753
FILING DATE: 22-Jan-2002
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 28758/33766
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856

INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 349 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: "CTGF amino acid sequence"
SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-10-053-753-8

Query Match   100.0%; Score 956; DB 4; Length 349;
Best Local Similarity 100.0%; Pred. No. 1.8e-83;
Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy    1 ALAAYRLEDTFGPDPTMIRANCLVQTTEWSACSKTCGMGISTRVTNDNASCRLEKQSRLC  60
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Db  178 ALAAYRLEDTFGPDPTMIRANCLVQTTEWSACSKTCGMGISTRVTNDNASCRLEKQSRLC 237

Qy   61 MVRPCEADLEENIKKGKKCIRTPKISKPIKFELSGCTSMKTYRAKFCGVCTDGRCCTPHR 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  238 MVRPCEADLEENIKKGKKCIRTPKISKPIKFELSGCTSMKTYRAKFCGVCTDGRCCTPHR 297

Qy  121 TTTLPVEFKCPDGEVMKKNMMFIKTCACHYNCPGDNDIFESLYYRKMYGDMA 172
        |||||||||||||||||||||||||||||||||||||||||||||||||||
Db  298 TTTLPVEFKCPDGEVMKKNMMFIKTCACHYNCPGDNDIFESLYYRKMYGDMA 349
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RESULT 6
US-10-060-036-173
Sequence 173, Application US/10060036
Publication No. US20030071144A1
GENERAL INFORMATION:
APPLICANT: Benson, Darin R.
APPLICANT: Kalos, Michael D.
APPLICANT: Lodes, Michael J.
APPLICANT: Persing, David H.
APPLICANT: Hepler, William T.
APPLICANT: Jiang, Yuqiu
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF PANCREATIC CANCER
FILE REFERENCE: 210121.566
CURRENT APPLICATION NUMBER: US/10/060,036
CURRENT FILING DATE: 2002-01-30
NUMBER OF SEQ ID NOS: 4560
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 173
LENGTH: 349
TYPE: PRT
ORGANISM: Homo sapiens
US-10-060-036-173

Query Match   100.0%; Score 956; DB 4; Length 349;
Best Local Similarity 100.0%; Pred. No. 1.8e-83;
Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy    1 ALAAYRLEDTFGPDPTMIRANCLVQTTEWSACSKTCGMGISTRVTNDNASCRLEKQSRLC  60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  178 ALAAYRLEDTFGPDPTMIRANCLVQTTEWSACSKTCGMGISTRVTNDNASCRLEKQSRLC 237

Qy   61 MVRPCEADLEENIKKGKKCIRTPKISKPIKFELSGCTSMKTYRAKFCGVCTDGRCCTPHR 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  238 MVRPCEADLEENIKKGKKCIRTPKISKPIKFELSGCTSMKTYRAKFCGVCTDGRCCTPHR 297

Qy  121 TTTLPVEFKCPDGEVMKKNMMFIKTCACHYNCPGDNDIFESLYYRKMYGDMA 172
        |||||||||||||||||||||||||||||||||||||||||||||||||||
Db  298 TTTLPVEFKCPDGEVMKKNMMFIKTCACHYNCPGDNDIFESLYYRKMYGDMA 349
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RESULT 7
US-10-171-311-46
Sequence 46, Application US/10171311
Publication No. US20030087270A1
GENERAL INFORMATION:
APPLICANT: Schlegel, Robert
APPLICANT: Chen, Yan
APPLICANT: Zhao, Xumei
APPLICANT: Monahan, John
APPLICANT: Kamatkar, Shubhangi
APPLICANT: Glatt, Karen
APPLICANT: Gannavarapu, Manjula
APPLICANT: Hoersh, Sebastian
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY
TITLE OF INVENTION: OF CERVICAL CANCER
FILE REFERENCE: MRI-035
CURRENT APPLICATION NUMBER: US/10/171,311
CURRENT FILING DATE: 2002-06-12
PRIOR APPLICATION NUMBER: US 60/298,159
PRIOR FILING DATE: 2001-06-13
PRIOR APPLICATION NUMBER: US 60/298,155
PRIOR FILING DATE: 2001-06-13
PRIOR APPLICATION NUMBER: US 60/335,936
PRIOR FILING DATE: 2001-11-14
NUMBER OF SEQ ID NOS: 238
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 46
LENGTH: 349
TYPE: PRT
ORGANISM: Homo sapiens
US-10-171-311-46

Query Match   100.0%; Score 956; DB 4; Length 349;
Best Local Similarity 100.0%; Pred. No. 1.8e-83;
Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy    1 ALAAYRLEDTFGPDPTMIRANCLVQTTEWSACSKTCGMGISTRVTNDNASCRLEKQSRLC  60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  178 ALAAYRLEDTFGPDPTMIRANCLVQTTEWSACSKTCGMGISTRVTNDNASCRLEKQSRLC 237

Qy   61 MVRPCEADLEENIKKGKKCIRTPKISKPIKFELSGCTSMKTYRAKFCGVCTDGRCCTPHR 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  238 MVRPCEADLEENIKKGKKCIRTPKISKPIKFELSGCTSMKTYRAKFCGVCTDGRCCTPHR 297

Qy  121 TTTLPVEFKCPDGEVMKKNMMFIKTCACHYNCPGDNDIFESLYYRKMYGDMA 172
        |||||||||||||||||||||||||||||||||||||||||||||||||||
Db  298 TTTLPVEFKCPDGEVMKKNMMFIKTCACHYNCPGDNDIFESLYYRKMYGDMA 349
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RESULT 8
US-10-205-823-78
; Sequence 78, Application US/10205823
; Publication No. US20030108963A1
US-10-205-823-78
GENERAL INFORMATION:
APPLICANT: Schlegel, Robert
APPLICANT: Monahan, John E.
APPLICANT: Endege, Wilson O.
APPLICANT: Gannavarapu, Manjula
APPLICANT: Gorbatcheva, Bella
APPLICANT: Hoersch, Sebastian
APPLICANT: Kamatkar, Shubhangi
APPLICANT: Wonsey, Angela M.
APPLICANT: Glatt, Karen
APPLICANT: Zhao, Xumei
APPLICANT: Anderson, Dustin
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS AND
TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
TITLE OF INVENTION: THERAPY OF PROSTATE CANCER
FILE REFERENCE: MRI-044
CURRENT APPLICATION NUMBER: US/10/205,823
CURRENT FILING DATE: 2002-07-25
PRIOR APPLICATION NUMBER: 60/307,982
PRIOR FILING DATE: 2001-07-25
PRIOR APPLICATION NUMBER: 60/314,356
PRIOR FILING DATE: 2001-08-22
PRIOR APPLICATION NUMBER: 60/325,020
PRIOR FILING DATE: 2001-09-25
PRIOR APPLICATION NUMBER: 60/341,746
PRIOR FILING DATE: 2001-12-12
PRIOR APPLICATION NUMBER: 60/362,158
PRIOR FILING DATE: 2002-03-05
NUMBER OF SEQ ID NOS: 455
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 78
LENGTH: 349
TYPE: PRT
ORGANISM: Homo sapiens
US-10-205-823-78

Query Match   100.0%; Score 956; DB 4; Length 349;
Best Local Similarity 100.0%; Pred. No. 1.8e-83;
Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   1 ALAAYRLEDTFGPDPTMIRANCLVQTTEWSACSKTCGMGISTRVTNDNASCRLEKQSRLC 60
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   178 ALAAYRLEDTFGPDPTMIRANCLVQTTEWSACSKTCGMGISTRVTNDNASCRLEKQSRLC 237

Qy   61 MVRPCEADLEENIKKGKKCCIRTPKISKPIKFELSGGCTSMKTYRAKFCGVCTDGRCCTPHR 120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   238 MVRPCEADLEENIKKGKKCCIRTPKISKPIKFELSGGCTSMKTYRAKFCGVCTDGRCCTPHR 297

Qy   121 TTTLPVEFKCPDGEVMKKNMMFIKTCACHYNCPGDNDIFESLYYRKMYGDMA 172
            ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   298 TTTLPVEFKCPDGEVMKKNMMFIKTCACHYNCPGDNDIFESLYYRKMYGDMA 349

RESULT 9
US-10-245-977-2
; Sequence 2, Application US/10245977
; Publication No. US20030113816A1
US-10-245-977-2
GENERAL INFORMATION:
APPLICANT: Weitz, Stephen L
APPLICANT: Usinger, William R
TITLE OF INVENTION: METHODS OF ASSAYING CONNECTIVE TISSUE GROWTH FACTOR
FILE REFERENCE: FP0812 US
CURRENT APPLICATION NUMBER: US/10/245,977
CURRENT FILING DATE: 2002-09-18
PRIOR APPLICATION NUMBER: US 60/323,305
PRIOR FILING DATE: 2001-09-18
NUMBER OF SEQ ID NOS: 8

SOFTWARE: Patentin version 3.1
SEQ ID NO 2
LENGTH: 349
TYPE: PRT
ORGANISM: Homo sapiens
US-10-245-977-2

Query Match   100.0%; Score 956; DB 4; Length 349;
Best Local Similarity 100.0%; Pred. No. 1.8e-83;
Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   1 ALAAYRLEDTFGPDPTMIRANCLVQTTEWSACSKTCGMGISTRVTNDNASCRLEKQSRLC 60
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Db   178 ALAAYRLEDTFGPDPTMIRANCLVQTTEWSACSKTCGMGISTRVTNDNASCRLEKQSRLC 237

Qy   61 MVRPCEADLEENIKKGKKCCIRTPKISKPIKFELSGGCTSMKTYRAKFCGVCTDGRCCTPHR 120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   238 MVRPCEADLEENIKKGKKCCIRTPKISKPIKFELSGGCTSMKTYRAKFCGVCTDGRCCTPHR 297

Qy   121 TTTLPVEFKCPDGEVMKKNMMFIKTCACHYNCPGDNDIFESLYYRKMYGDMA 172
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Db   298 TTTLPVEFKCPDGEVMKKNMMFIKTCACHYNCPGDNDIFESLYYRKMYGDMA 349

RESULT 10
US-10-315-568-2
; Sequence 2, Application US/10315568
; Publication No. US20030180300A1
US-10-315-568-2
GENERAL INFORMATION:
APPLICANT: FibroGen, Inc.
APPLICANT: Grotendorst, Gary R.
TITLE OF INVENTION: CONNECTIVE TISSUE GROWTH FACTOR FRAGMENTS AND METHODS AND USES TH
FILE REFERENCE: FIBRO1140-3
CURRENT APPLICATION NUMBER: US/10/315,568
CURRENT FILING DATE: 2002-12-09
PRIOR APPLICATION NUMBER: US 09/461,688
PRIOR FILING DATE: 1999-12-14
PRIOR APPLICATION NUMBER: US 60/112,240
PRIOR FILING DATE: 1998-12-14
PRIOR APPLICATION NUMBER: US 60/112,241
PRIOR FILING DATE: 1998-12-14
NUMBER OF SEQ ID NOS: 4
SOFTWARE: Patentin version 3.0
SEQ ID NO 2
LENGTH: 349
TYPE: PRT
ORGANISM: Homo sapiens
US-10-315-568-2

Query Match   100.0%; Score 956; DB 4; Length 349;
Best Local Similarity 100.0%; Pred. No. 1.8e-83;
Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db   178 ALAAYRLEDTFGPDPTMIRANCLVQTTEWSACSKTCGMGISTRVTNDNASCRLEKQSRLC 237

Qy   61 MVRPCEADLEENIKKGKKCCIRTPKISKPIKFELSGGCTSMKTYRAKFCGVCTDGRCCTPHR 120
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Qy   121 TTTLPVEFKCPDGEVMKKNMMFIKTCACHYNCPGDNDIFESLYYRKMYGDMA 172
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Db   298 TTTLPVEFKCPDGEVMKKNMMFIKTCACHYNCPGDNDIFESLYYRKMYGDMA 349

RESULT 11
US-10-394-015-4
; Sequence 4, Application US/10394015
; Publication No. US20030180891A1
GENERAL INFORMATION:
APPLICANT: Young, Paul
APPLICANT: Ruben, Steven M.

; TITLE OF INVENTION: Connective Tissue Growth Factor-4
; FILE REFERENCE: PF467
; CURRENT APPLICATION NUMBER: US/10/394,015
; CURRENT FILING DATE: 2003-03-24
; PRIOR APPLICATION NUMBER: US/09/325,019
; PRIOR FILING DATE: 1999-06-03
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/088,320
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-05
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Patentin Ver. 2.0
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; SEQ ID NO 4
; LENGTH: 349
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-394-015-4

Query Match   100.0%; Score 956; DB 4; Length 349;
Best Local Similarity 100.0%; Pred. No. 1.8e-83;
Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy   61 MVRPCEADLEENIKKGKKCIRTPKISKPIKFELSGCTSMKTYRAKFCGVCTDGRCCTPHR 120
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Qy   121 TTTLPVEFKCPDGEVMKKNMMFIKTCACHYNCPGDNDIFESLYYRKMYGDMA 172
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Db   298 TTTLPVEFKCPDGEVMKKNMMFIKTCACHYNCPGDNDIFESLYYRKMYGDMA 349

RESULT 12
US-10-131-985-7
; Sequence 7, Application US/10131985
; Publication No. US20030194440A1
; GENERAL INFORMATION:
; APPLICANT: Deck, Kevin N
; APPLICANT: Davies, Michael J
; APPLICANT: Fish, Paul V
; APPLICANT: Huggins, Jonathan P
; APPLICANT: McIntosh, Fraser S
; APPLICANT: Occleston, Nicholas L
; TITLE OF INVENTION: Composition
; FILE REFERENCE: PCS 10391A
; CURRENT APPLICATION NUMBER: US/10/131,985
; CURRENT FILING DATE: 2002-04-25
; PRIOR APPLICATION NUMBER: US/09/726,295
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: GB 9930768.8
; PRIOR FILING DATE: 1999-12-29
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: Patentin Ver. 2.1
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; SEQ ID NO 7
; LENGTH: 349
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-131-985-7

Query Match   100.0%; Score 956; DB 4; Length 349;
Best Local Similarity 100.0%; Pred. No. 1.8e-83;
Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db   178 ALAAYRLEDTFGPDPTMIRANCLVQTTEWSACSKTCGMGISTRVTNDNASCRLEKQSRLC 237

Qy   61 MVRPCEADLEENIKKGKKCIRTPKISKPIKFELSGCTSMKTYRAKFCGVCTDGRCCTPHR 120
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Db   238 MVRPCEADLEENIKKGKKCIRTPKISKPIKFELSGCTSMKTYRAKFCGVCTDGRCCTPHR 297

Qy   121 TTTLPVEFKCPDGEVMKKNMMFIKTCACHYNCPGDNDIFESLYYRKMYGDMA 172
            |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   298 TTTLPVEFKCPDGEVMKKNMMFIKTCACHYNCPGDNDIFESLYYRKMYGDMA 349

RESULT 13
US-10-182-432-8
; Sequence 8, Application US/10182432
; Publication No. US20040002124A1
; GENERAL INFORMATION:
; APPLICANT: LAU, Lester F., YEUNG, Cho-Yau, and GREENSPAN, Jeffrey A.
; TITLE OF INVENTION: CYR61 COMPOSITIONS AND METHODS
; FILE REFERENCE: 214448/00029
; CURRENT APPLICATION NUMBER: US/10/182,432
; CURRENT FILING DATE: 2002-07-26
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: Patentin Ver. 2.0
;
; SEQ ID NO 8
; LENGTH: 349
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-182-432-8

Query Match   100.0%; Score 956; DB 4; Length 349;
Best Local Similarity 100.0%; Pred. No. 1.8e-83;
Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy   121 TTTLPVEFKCPDGEVMKKNMMFIKTCACHYNCPGDNDIFESLYYRKMYGDMA 172
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RESULT 14
US-10-338-587A-2
; Sequence 2, Application US/10338587A
; Publication No. US20040005319A1
; GENERAL INFORMATION:
; APPLICANT: THE UNIVERSITY OF SOUTH FLORIDA
; APPLICANT: GROTENDORST, Gary R.
; APPLICANT: BRADHAM, Douglass M.
; TITLE OF INVENTION: CONNECTIVE TISSUE GROWTH FACTOR
; FILE REFERENCE: USF1100-15
; CURRENT APPLICATION NUMBER: US/10/338,587A
; CURRENT FILING DATE: 2003-01-07
; PRIOR APPLICATION NUMBER: US 09/054,363
; PRIOR FILING DATE: 1998-04-02
; PRIOR APPLICATION NUMBER: US 08/459,717
; PRIOR FILING DATE: 1995-06-02
; PRIOR APPLICATION NUMBER: US 08/386,680
; PRIOR FILING DATE: 1995-02-10
; PRIOR APPLICATION NUMBER: US 08/167,628
; PRIOR FILING DATE: 1993-12-14
; PRIOR APPLICATION NUMBER: US 07/752,427
; PRIOR FILING DATE: 1991-08-30
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: Patentin version 3.1
;
; SEQ ID NO 2
; LENGTH: 349
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-338-587A-2

Query Match   100.0%; Score 956; DB 4; Length 349;
Best Local Similarity 100.0%; Pred. No. 1.8e-83;
Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy   121 TTTLPVEFKCPDGEVMKKNMMFIKTCACHYNCPGDNDIFESLYYRKMYGDMA 172
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Qy       61 MVRPCEADLEENIKKGKKCIRTPKISKPIKFELSGGCTSMKTYRAKFCGVCTDGRCCTPHR  120
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Db      238 MVRPCEADLEENIKKGKKCIRTPKISKPIKFELSGGCTSMKTYRAKFCGVCTDGRCCTPHR  297

Qy      121 TTTLPVEFKCPDGEVMKKNMMFIKTCACHYNCPGDNDIFESLYYRKMYGDMA  172
            |||||||||||||||||||||||||||||||||||||||||||||||||||
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RESULT 15
US-10-428-487-44
; Sequence 44, Application US/10428487
; Publication No. US20040006780A1
; GENERAL INFORMATION:
; APPLICANT: RASTELLI, LUCA K.
; APPLICANT: GERBER, HANS-PETER
; TITLE OF INVENTION: VEGF-MODULATED GENES AND METHODS EMPLOYING THEM
; FILE REFERENCE: 09800080-0103
; CURRENT APPLICATION NUMBER: US/10/428,487
; CURRENT FILING DATE: 2003-05-02
; PRIOR APPLICATION NUMBER: 09/815,153
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,201
; PRIOR FILING DATE: 2000-03-22
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 44
;   LENGTH: 349
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-428-487-44

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Qy      121 TTTLPVEFKCPDGEVMKKNMMFIKTCACHYNCPGDNDIFESLYYRKMYGDMA  172
            |||||||||||||||||||||||||||||||||||||||||||||||||||
Db      298 TTTLPVEFKCPDGEVMKKNMMFIKTCACHYNCPGDNDIFESLYYRKMYGDMA  349
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Search completed: January   9, 2006, 11:30:43
Job time : 116 secs

November 2005

Published_Applications Nucleic Acid and Published_Applications Amino Acid database searches now generate two sets of results each. The Published_Applications databases have been split into two parts to reduce the amount of time required for their daily updates. This results in more machine time being available for processing searches.

Newly published applications will appear in the Published_Applications_New databases: older published applications make up the Published_Applications_Main databases.

Searches run against Nucleic Acid Published_Applications produce two sets of results, with the extensions **.rnpbn** (Published_Applications_NA_Main) and **.rnpbn** (Published_Applications_NA_New)

Searches run against Amino Acid Published_Applications produce two sets of results, with the extensions **.rapbn** (Published_Applications_AA_Main) and **.rapbn** (Published_Applications_AA_New).

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OM protein - protein search, using sw model

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GenCore version 5.1.6

Run on: January 9, 2006, 11:20:03

Title: US-09-461-646-4
Perfect score: 956
Sequence: 1 ALAAYRLEDTFGPDPTMIRA..........PGDNDIFESLYYRKMYGDMA 172

Scoring table: BLOSUM62
                 Gapop 10.0 , Gapext 0.5

Searched: 61141 seqs, 8493638 residues

Total number of hits satisfying chosen parameters: 61141

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Published Applications AA_New:*
                 1: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
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                 (without alignments)

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	956	100.0	349	7	US-11-067-121-14	Sequence 14, Appl
2	956	100.0	397	6	US-10-821-234-1020	Sequence 1020, Ap
3	934	97.7	348	7	US-11-067-121-5	Sequence 5, Appl
4	925	96.8	317	7	US-11-094-519A-38	Sequence 38, Appl
5	848	88.7	322	7	US-11-067-121-15	Sequence 15, Appl
6	432	45.2	74	7	US-11-094-519A-46	Sequence 46, Appl
7	148	15.5	250	6	US-10-131-826A-320	Sequence 320, App
8	103.5	10.8	1216	7	US-11-039-398-8	Sequence 8, Appl
9	103.5	10.8	1222	7	US-11-039-398-12	Sequence 12, Appl
10	103.5	10.8	1235	7	US-11-039-398-16	Sequence 16, Appl
11	103.5	10.8	1252	7	US-11-039-398-20	Sequence 20, Appl
12	102	10.7	1213	7	US-11-039-398-14	Sequence 14, Appl
13	102	10.7	1219	7	US-11-039-398-10	Sequence 10, Appl
14	102	10.7	1232	7	US-11-039-398-18	Sequence 18, Appl
15	102	10.7	1249	7	US-11-039-398-22	Sequence 22, Appl
16	94.5	9.9	1210	6	US-10-624-932-26	Sequence 26, Appl
17	94.5	9.9	1454	7	US-11-109-157A-2	Sequence 2, Appl
18	94.5	9.9	1686	7	US-11-109-157A-1	Sequence 1, Appl
19	89	9.3	938	7	US-11-109-157A-18	Sequence 18, Appl
20	89	9.3	1221	7	US-11-109-157A-17	Sequence 17, Appl
21	87.5	9.2	386	7	US-11-143-986-3	Sequence 3, Appli
22	87.5	9.2	386	7	US-11-143-986-2	Sequence 2, Appli
23	87	9.1	1170	6	US-10-831-997-2	Sequence 2, Appl
24	87	9.1	1170	6	US-10-995-561-594	Sequence 594, App
25	87	9.1	1170	6	US-10-995-561-595	Sequence 595, App
26	87	9.1	1170	6	US-10-995-561-596	Sequence 596, App
27	87	9.1	1170	7	US-11-046-456-28	Sequence 28, Appl
28	87	9.1	1170	7	US-11-046-644-28	Sequence 28, Appl
29	86.5	9.0	69	7	US-11-022-562-224	Sequence 224, App
30	86.5	9.0	1211	7	US-11-022-562-224	Sequence 224, App
31	84.5	8.8	372	7	US-11-143-986-4	Sequence 4, Appli
32	84.5	8.8	372	7	US-11-143-986-6	Sequence 6, Appli
33	84.5	8.8	397	7	US-11-022-562-223	Sequence 223, App
34	82	8.6	1907	7	US-11-039-398-25	Sequence 25, Appl
35	81.5	8.5	2515	7	US-11-113-424-53	Sequence 53, Appl
36	81.5	8.5	4655	6	US-10-995-561-556	Sequence 556, App
37	81	8.5	795	7	US-11-109-157A-14	Sequence 14, Appl
38	81	8.5	1072	7	US-11-109-157A-13	Sequence 13, Appl
39	81	8.5	1172	7	US-11-186-284-203	Sequence 203, App
40	79.5	8.3	5179	7	US-11-108-172-1068	Sequence 1068, Ap
41	79	8.3	2764	6	US-10-995-561-691	Sequence 691, App
42	79	8.3	2813	6	US-10-995-561-688	Sequence 688, App
43	79	8.3	2919	6	US-10-821-234-1133	Sequence 1133, Ap
44	76.5	8.0	335	7	US-11-136-619-30	Sequence 30, Appl
45	76.5	8.0	351	7	US-11-136-619-14	Sequence 14, Appl

ALIGNMENTS

RESULT 1
US-11-067-121-14
; Sequence 14, Application US/11067121
; Publication No. US2005026118SA1
; GENERAL INFORMATION:
; APPLICANT: Martijn;
; APPLICANT: Rondahl, Lena
; APPLICANT: Martijn, Cecile
; TITLE OF INVENTION: THERAPEUTIC PROTEINS
; FILE REFERENCE: 18909-002001
; CURRENT APPLICATION NUMBER: US/11/067,121
; CURRENT FILING DATE: 2005-02-25
; PRIOR APPLICATION NUMBER: US 60/576,445
; PRIOR FILING DATE: 2004-06-02
; PRIOR APPLICATION NUMBER: SE 0400489-1
; PRIOR FILING DATE: 2004-02-27
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 349
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-067-121-14

Query Match   100.0%; Score 956; DB 7; Length 349;
Best Local Similarity   100.0%; Pred. No. 1.3e-88;
Matches   172; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

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RESULT 2
US-10-821-234-1020
; Sequence 1020, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan

; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER:
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt_SEQ_genes Version 1.0
; SEQ ID NO 1020
; TYPE: PRT
; LENGTH: 397
; ORGANISM: Homo sapiens
US-10-821-234-1020

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Db 286 MVRPCEADLEENIKKGKKCCIRTPKISKPIKFELSGCTSMKTYRAKFCGVCTDGRCCTPHR 345

Qy 121 TTTLPVEFKCPDGEVMKKNMMFIKTCACHYNCPGDNDIFESLYYRKMYGDMA 172
         |||||||||||||||||||||||||||||||||||||||||||||||||||
Db 346 TTTLPVEFKCPDGEVMKKNMMFIKTCACHYNCPGDNDIFESLYYRKMYGDMA 397

RESULT 3
US-11-067-121-5
; Sequence 5, Application US/11067121
; Publication No. US20050261185A1
; GENERAL INFORMATION:
; APPLICANT: Martijn, Cecile
; APPLICANT: Rondahl, Lena
; TITLE OF INVENTION: THERAPEUTIC PROTEINS
; FILE REFERENCE: 18909-002001
; CURRENT APPLICATION NUMBER: US/11/067,121
; CURRENT FILING DATE: 2005-02-25
; PRIOR APPLICATION NUMBER: US 60/576,445
; PRIOR FILING DATE: 2004-06-02
; PRIOR APPLICATION NUMBER: SE 0400489-1
; PRIOR FILING DATE: 2004-02-27
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 348
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-067-121-5

Query Match   97.7%; Score 934; DB 7; Length 348;
Best Local Similarity   95.9%; Pred. No. 2e-86;
Matches 165; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Qy   1 ALAAYRLEDTFGPDPTMIRANCLVQTTEWSACSKTCGMGISTRVTNDNTFCRLEKQSRLC 60
         ||||||||||||||||||||||||||||||||||||||||||| ||:||||||||
Db 177 ALAAYRLEDTFGPDPTMIRANCLVQTTEWSACSKTCGMGISTRVTNDNTFCRLEKQSRLC 236

Qy   61 MVRPCEADLEENIKKGKKCCIRTPKISKPIKFELSGCTSMKTYRAKFCGVCTDGRCCTPHR 120
         |||||||||||||||||||||||||||| ||:|||||||||||||||||||||||||
Db 237 MVRPCEADLEENIKKGKKCCIRTPKIAKPVKFELSGCTSVKTYRAKFCGVCTDGRCCTPHR 296

Qy 121 TTTLPVEFKCPDGEVMKKNMMFIKTCACHYNCPGDNDIFESLYYRKMYGDMA 172
         |||||||||||||:|||||||||||||||||||||||||||||||||||||
Db 297 TTTLPVEFKCPDGEIMKKNMFIKTCACHYNCPGDNDIFESLYYRKMYGDMA 348

US-11-094-519A-38
; Sequence 38, Application US/11094519A
; Publication No. US20050281810A1
; GENERAL INFORMATION:
; APPLICANT: LEVINE, Zurit
; APPLICANT: BERNSTEIN, Jeanne
; TITLE OF INVENTION: VARIANTS OF ALTERNATIVE SPLICING
; FILE REFERENCE: 2786-0140P
; CURRENT APPLICATION NUMBER: US/11/094,519A
; CURRENT FILING DATE: 2005-03-31
; PRIOR APPLICATION NUMBER: US/09/695,293
; PRIOR FILING DATE: 2000-10-25
; PRIOR APPLICATION NUMBER: IL 132558
; PRIOR FILING DATE: 1999-10-25
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 38
; LENGTH: 317
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-094-519A-38

Query Match   96.8%; Score 925; DB 7; Length 317;
Best Local Similarity   99.4%; Pred. No. 1.4e-85;
Matches 165; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy   7 LEDTFGPDPTMIRANCLVQTTEWSACSKTCGMGISTRVTNDNASCRLEKQSRLCMVRPCE 66
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 152 LEDTFGPDPTMIRANCLVQTTEWSACSKTCGMGISTRVTNDNASCRLEKQSRLCMVRPCE 211

Qy   67 ADLEENIKKGKKCCIRTPKISKPIKFELSGCTSMKTYRAKFCGVCTDGRCCTPHRTTTLPV 126
         :|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 212 SDLEENIKKGKKCCIRTPKISKPIKFELSGCTSMKTYRAKFCGVCTDGRCCTPHRTTTLPV 271

Qy 127 EFKCPDGEVMKKNMMFIKTCACHYNCPGDNDIFESLYYRKMYGDMA 172
         ||||||||||||||||||||||||||||||||||||||||||||||
Db 272 EFKCPDGEVMKKNMMFIKTCACHYNCPGDNDIFESLYYRKMYGDMA 317

RESULT 5
US-11-067-121-15
; Sequence 15, Application US/11067121
; Publication No. US20050261185A1
; GENERAL INFORMATION:
; APPLICANT: Martijn, Cecile
; APPLICANT: Rondahl, Lena
; TITLE OF INVENTION: THERAPEUTIC PROTEINS
; FILE REFERENCE: 18909-002001
; CURRENT APPLICATION NUMBER: US/11/067,121
; CURRENT FILING DATE: 2005-02-25
; PRIOR APPLICATION NUMBER: US 60/576,445
; PRIOR FILING DATE: 2004-06-02
; PRIOR APPLICATION NUMBER: SE 0400489-1
; PRIOR FILING DATE: 2004-02-27
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 322
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-067-121-15

Query Match   88.7%; Score 848; DB 7; Length 322;
Best Local Similarity   99.3%; Pred. No. 7.2e-78;
Matches 151; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy   21 NCLVQTTEWSACSKTCGMGISTRVTNDNASCRLEKQSRLCMVRPCEADLEENIKKGKKCCI 80
         :|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 171 DCLVQTTEWSACSKTCGMGISTRVTNDNASCRLEKQSRLCMVRPCEADLEENIKKGKKCCI 230

Qy   81 RTPKISKPIKFELSGCTSMKTYRAKFCGVCTDGRCCTPHRTTTLPVEFKCPDGEVMKKNM 140
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 231 RTPKISKPIKFELSGCTSMKTYRAKFCGVCTDGRCCTPHRTTTLPVEFKCPDGEVMKKNM 290

RESULT 4

```
Qy          141  MFIKTCACHYNCPGDNDIFESLYYRKMYGDMA 172
                 ||||||||||||||||||||||||||||||||
Db          291  MFIKTCACHYNCPGDNDIFESLYYRKMYGDMA 322


RESULT 6
US-11-094-519A-46
; Sequence 46, Application US/11094519A
; Publication No. US20050281810A1
; GENERAL INFORMATION:
;  APPLICANT: LEVINE, Zurit
;  APPLICANT: BERNSTEIN, Jeanne
;  TITLE OF INVENTION: VARIANTS OF ALTERNATIVE SPLICING
;  FILE REFERENCE: 2786-0140P
;  CURRENT APPLICATION NUMBER: US/11/094,519A
;  CURRENT FILING DATE: 2005-03-31
;  PRIOR APPLICATION NUMBER: US/09/695,293
;  PRIOR FILING DATE: 2000-10-25
;  PRIOR APPLICATION NUMBER: IL 132558
;  PRIOR FILING DATE: 1999-10-25
;  NUMBER OF SEQ ID NOS: 52
;  SOFTWARE: Patentin Ver. 2.1
;  SEQ ID NO 46
;    LENGTH: 74
;    TYPE: PRT
;    ORGANISM: Homo sapiens
US-11-094-519A-46

Query Match             45.2%;  Score 432;  DB 7;  Length 74;
Best Local Similarity  100.0%;  Pred. No. 5.3e-37;
Matches   74;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy           99  MKTYRAKFCGVCTDGRCCTPHRTTTLPVEFKCPDGEVMKKNMMFIKTCACHYNCPGDNDI 158
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db            1  MKTYRAKFCGVCTDGRCCTPHRTTTLPVEFKCPDGEVMKKNMMFIKTCACHYNCPGDNDI 60

Qy          159  FESLYYRKMYGDMA 172
                 ||||||||||||||
Db           61  FESLYYRKMYGDMA 74


RESULT 7
US-10-131-826A-320
; Sequence 320, Application US/10131826A
; Publication No. US20050245730A1
; GENERAL INFORMATION:
;  APPLICANT: Baker,Kevin P.
;  APPLICANT: Bereini,Maureen
;  APPLICANT: DeForge,Laura
;  APPLICANT: Desnoyers,Luc
;  APPLICANT: Filvaroff,Ellen
;  APPLICANT: Gao,Wei-Qiang
;  APPLICANT: Gerritsen,Mary E.
;  APPLICANT: Goddard,Audrey
;  APPLICANT: Godowski,Paul J.
;  APPLICANT: Gurney,Austin L.
;  APPLICANT: Sherwood,Steven
;  APPLICANT: Smith,Victoria
;  APPLICANT: Stewart,Timothy A.
;  APPLICANT: Tumas,Daniel
;  APPLICANT: Watanabe,Colin K
;  APPLICANT: Wood,William
;  APPLICANT: Zhang, Zemin
;  TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;  TITLE OF INVENTION: ACIDS ENCODING THE SAME
;  FILE REFERENCE: P3330RIC128
;  CURRENT APPLICATION NUMBER: US/10/131,826A
;  CURRENT FILING DATE: 2002-04-24
;  PRIOR APPLICATION NUMBER: 60/049911
;  PRIOR FILING DATE: 1997-06-18
;  PRIOR APPLICATION NUMBER: 60/056974
;  PRIOR FILING DATE: 1997-08-26
```

```
;  PRIOR APPLICATION NUMBER: 60/059113
;  PRIOR FILING DATE: 1997-09-17
;  PRIOR APPLICATION NUMBER: 60/059115
;  PRIOR FILING DATE: 1997-09-17
;  PRIOR APPLICATION NUMBER: 60/059117
;  PRIOR FILING DATE: 1997-09-17
;  PRIOR APPLICATION NUMBER: 60/059122
;  PRIOR FILING DATE: 1997-09-17
;  PRIOR APPLICATION NUMBER: 60/059184
;  PRIOR FILING DATE: 1997-09-17
;  PRIOR APPLICATION NUMBER: 60/059263
;  PRIOR FILING DATE: 1997-09-18
;  PRIOR APPLICATION NUMBER: 60/059352
;  PRIOR FILING DATE: 1997-09-19
;  PRIOR APPLICATION NUMBER: 60/059588
;  PRIOR FILING DATE: 1997-09-19
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 550
;  SEQ ID NO 320
;    LENGTH: 250
;    TYPE: PRT
;    ORGANISM: Homo Sapien
US-10-131-826A-320

Query Match             15.5%;  Score 148;  DB 6;  Length 250;
Best Local Similarity   56.8%;  Pred. No. 4.3e-08;
Matches   25;  Conservative   6;  Mismatches  13;  Indels   0;  Gaps   0;

Qy           22  CLVQTTEWSACSKTCGMGISTRVTNDNASCRLEKQSRLCMVRPC 65
                 | : || ||| | :|| :|| | || | | ||||| : |||||| |||
Db          194  CPEWSTAWGPCSTTCGLGMATRVSNQNRFCRLETQRRLCISRPC 237


RESULT 8
US-11-039-398-12
; Sequence 12, Application US/11039398
; Publication No. US20050267297A1
; GENERAL INFORMATION:
;  APPLICANT: Friddle, Carl Johan
;  APPLICANT: Turner, C. Alexander Jr.
;  APPLICANT: Walke, D. Wade
;  APPLICANT: Hilbun, Erin
;  APPLICANT: Nepomnichy, Boris
;  APPLICANT: Hu, Yi
;  TITLE OF INVENTION: Novel Human Proteases and
;  TITLE OF INVENTION: Polynucleotides Encoding the Same
;  FILE REFERENCE: LEX-0221-USA
;  CURRENT APPLICATION NUMBER: US/11/039,398
;  CURRENT FILING DATE: 2005-01-20
;  PRIOR APPLICATION NUMBER: US/09/938,330
;  PRIOR FILING DATE: 2001-08-22
;  PRIOR APPLICATION NUMBER: US 60/227,104
;  PRIOR FILING DATE: 2000-08-22
;  PRIOR APPLICATION NUMBER: US 60/233,796
;  PRIOR FILING DATE: 2000-09-19
;  NUMBER OF SEQ ID NOS: 26
;  SOFTWARE: FastSEQ for Windows Version 4.0
;  SEQ ID NO 12
;    LENGTH: 1216
;    TYPE: PRT
;    ORGANISM: homo sapiens
US-11-039-398-12

Query Match             10.8%;  Score 103.5;  DB 7;  Length 1216;
Best Local Similarity   22.6%;  Pred. No. 0.0061;
Matches   45;  Conservative  24;  Mismatches  57;  Indels  73;  Gaps  11;

Qy           15  PTMIRANC------------LVQTTEWSACSKTCG-MGISTRVTNDNASCRLEKQSRLCMVRPC 65
                 | | |||          || | ||||||| | : | :|| |:|| | || | | |||||:|||||||
Db          894  PKPIRRRCNQHPCSQPVWVTEEWGACSRSCGKLGVQTR-----GIQCLLPLSNGTHKVMPA 949

Qy           66  EADLEENIKGKKCIRTPKISKPIKFEL---SGCTSMKTYRAKFCG----------------- 108
                 :|:||         |:||                |:|
```

RESULT 9
US-11-039-398-8
; Sequence 8, Application US/11039398
; Publication No. US20050267297A1
; GENERAL INFORMATION:
; APPLICANT: Friddle, Carl Johan
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Walke, D. Wade
; APPLICANT: Hilbun, Erin
; APPLICANT: Nepomnichy, Boris
; APPLICANT: Hu, Yi
; TITLE OF INVENTION: Novel Human Proteases and
; TITLE OF INVENTION: Polynucleotides Encoding the Same
; FILE REFERENCE: LEX-0221-USA
; CURRENT APPLICATION NUMBER: US/11/039,398
; CURRENT FILING DATE: 2005-01-20
; PRIOR APPLICATION NUMBER: US/09/938,330
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: US 60/227,104
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: US 60/233,796
; PRIOR FILING DATE: 2000-09-19
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 1222
; TYPE: PRT
; ORGANISM: homo sapiens
US-11-039-398-8

Query Match   10.8%; Score 103.5; DB 7; Length 1222;
Best Local Similarity   22.6%; Pred. No. 0.0062;
Matches   45; Conservative   24; Mismatches   57; Indels   73; Gaps   11;

```
Qy     15 PTMIRANC-------LVQTTEWSACSKTCG-MGISTRVTNDNASCRLEKQSRLCMVRPC  65
                      :||:|  |: | :|||:||
Db    894 PKPIRRRCNQHPCSQPVWTEEWGACSRSCCKLGVQTR----GIQCLLPLSNGTHKVMPA 949

Qy     66 EADLEENIKGKKCCIRTPKISKPIKFEL---SGCTSMKTYRAKFCG------------- 108
Db    950 KACAGDRPEARRPCLRVP---CPAQWRLGAWSQCSAT------CGEGIQORQVVCRTNA 999

Qy    109 -------------VCTDGRCCTPHRTTTLPV---EFKCPDGE--------VMKKNM 140
Db   1000 NSLGHCEGDRPDTVQVCSLPACGGNHQNSTVRADVWELGTPEGQWVPQSGPLHPINKISS 1059

Qy    141 MFIKTCACHYNCPGDNDIF 159
Db   1060 M----CAAE-PCTGDRSVF 1073
```

RESULT 10
US-11-039-398-16
; Sequence 16, Application US/11039398
; Publication No. US20050267297A1
; GENERAL INFORMATION:
; APPLICANT: Friddle, Carl Johan
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Walke, D. Wade
; APPLICANT: Hilbun, Erin
; APPLICANT: Nepomnichy, Boris
; APPLICANT: Hu, Yi
; TITLE OF INVENTION: Novel Human Proteases and
; TITLE OF INVENTION: Polynucleotides Encoding the Same
; FILE REFERENCE: LEX-0221-USA
; CURRENT APPLICATION NUMBER: US/11/039,398
; CURRENT FILING DATE: 2005-01-20
; PRIOR APPLICATION NUMBER: US/09/938,330
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: US 60/227,104
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: US 60/233,796
; PRIOR FILING DATE: 2000-09-19
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 1235
; TYPE: PRT
; ORGANISM: homo sapiens
US-11-039-398-16

Query Match   10.8%; Score 103.5; DB 7; Length 1235;
Best Local Similarity   22.6%; Pred. No. 0.0062;
Matches   45; Conservative   24; Mismatches   57; Indels   73; Gaps   11;

```
Qy     15 PTMIRANC-------LVQTTEWSACSKTCG-MGISTRVTNDNASCRLEKQSRLCMVRPC  65
Db    894 PKPIRRRCNQHPCSQPVWTEEWGACSRSCCKLGVQTR----GIQCLLPLSNGTHKVMPA 949

Qy     66 EADLEENIKGKKCCIRTPKISKPIKFEL---SGCTSMKTYRAKFCG------------- 108
Db    950 KACAGDRPEARRPCLRVP---CPAQWRLGAWSQCSAT------CGEGIQORQVVCRTNA 999

Qy    109 -------------VCTDGRCCTPHRTTTLPV---EFKCPDGE--------VMKKNM 140
Db   1000 NSLGHCEGDRPDTVQVCSLPACGGNHQNSTVRADVWELGTPEGQWVPQSGPLHPINKISS 1059

Qy    141 MFIKTCACHYNCPGDNDIF 159
Db   1060 M----CAAE-PCTGDRSVF 1073
```

RESULT 11
US-11-039-398-20
; Sequence 20, Application US/11039398
; Publication No. US20050267297A1
; GENERAL INFORMATION:
; APPLICANT: Friddle, Carl Johan
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Walke, D. Wade
; APPLICANT: Hilbun, Erin
; APPLICANT: Nepomnichy, Boris
; APPLICANT: Hu, Yi
; TITLE OF INVENTION: Novel Human Proteases and
; TITLE OF INVENTION: Polynucleotides Encoding the Same
; FILE REFERENCE: LEX-0221-USA
; CURRENT APPLICATION NUMBER: US/11/039,398
; CURRENT FILING DATE: 2005-01-20
; PRIOR APPLICATION NUMBER: US/09/938,330
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: US 60/227,104
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: US 60/233,796
; PRIOR FILING DATE: 2000-09-19
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 1252
; TYPE: PRT
; ORGANISM: homo sapiens
US-11-039-398-20

Query Match   10.8%; Score 103.5; DB 7; Length 1252;
Best Local Similarity   22.6%; Pred. No. 0.0063;
Matches   45; Conservative   24; Mismatches   57; Indels   73; Gaps   11;

RESULT 12
US-11-039-398-14
; Sequence 14, Application US/11039398
; Publication No. US20050267297A1
; GENERAL INFORMATION:
; APPLICANT: Friddle, Carl Johan
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Walke, D. Wade
; APPLICANT: Hilbun, Erin
; APPLICANT: Nepomnichy, Boris
; APPLICANT: Hu, Yi
; TITLE OF INVENTION: Novel Human Proteases and
; TITLE OF INVENTION: Polynucleotides Encoding the Same
; FILE REFERENCE: LEX-0221-USA
; CURRENT APPLICATION NUMBER: US/11/039,398
; CURRENT FILING DATE: 2005-01-20
; PRIOR APPLICATION NUMBER: US/09/938,330
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: US 60/227,104
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: US 60/233,796
; PRIOR FILING DATE: 2000-09-19
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 1213
; TYPE: PRT
; ORGANISM: homo sapiens
US-11-039-398-14

Query Match   10.7%; Score 102; DB 7; Length 1213;
Best Local Similarity   22.0%; Pred. No. 0.0087;
Matches   42; Conservative 27; Mismatches 62; Indels 60; Gaps 9;

```
Qy    15 PTMIRANC-------------LVQTTEWSACSKTCG-MGISTRVTNDNASCRLEKQSRLCMVRPC 65
                            |:| ||| : | ||| ||:||:||||:|:||||||:||::|
Db   894 PKPIRRRCNQHPCSQPVVWTEEWGACSRSCGKLGVQTR---GIQCLLPLSNGTHKVMPA 949

Qy    66 EADLEENIKKGKKCIRTPKISKPIKFEL----SGCTSMKTYRAKFCG------------- 108
                      ::    |::    |  | :::::||:||||   |
Db   950 KACAGDRPEARRPCLRVP---CPAQWRLGAWSQCSAT-------CGEGIQORQVVCRTNA 999

Qy   109 -------------VCTDGRCCTPHRTTLPV---EFKCPDGE------------VMKQNM 140
                          :||:  | :: | | ||
Db  1000 NSLGHCEGDRPDTVQVCSLPACGGNHQNSTVRADVWELGTPEGQWVPQSGPLHPINKISS 1059

Qy   141 MFIKTCACHYNCPGDNDIF 159
            | | |||||:||||
Db  1060 M----CAAE-PCTGDRSVF 1073
```

RESULT 13
US-11-039-398-10
; Sequence 10, Application US/11039398.
; Publication No. US20050267297A1

GENERAL INFORMATION:
; APPLICANT: Friddle, Carl Johan
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Walke, D. Wade
; APPLICANT: Hilbun, Erin
; APPLICANT: Nepomnichy, Boris
; APPLICANT: Hu, Yi
; TITLE OF INVENTION: Novel Human Proteases and
; TITLE OF INVENTION: Polynucleotides Encoding the Same
; FILE REFERENCE: LEX-0221-USA
; CURRENT APPLICATION NUMBER: US/11/039,398
; CURRENT FILING DATE: 2005-01-20
; PRIOR APPLICATION NUMBER: US/09/938,330
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: US 60/227,104
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: US 60/233,796
; PRIOR FILING DATE: 2000-09-19
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 1219
; TYPE: PRT
; ORGANISM: homo sapiens
US-11-039-398-10

Query Match   10.7%; Score 102; DB 7; Length 1219;
Best Local Similarity   22.0%; Pred. No. 0.0087;
Matches   42; Conservative 27; Mismatches 62; Indels 60; Gaps 9;

```
Qy    15 PTMIRANC-------------LVQTTEWSACSKTCG-MGISTRVTNDNASCRLEKQSRLCMVRPC 65
                            |:| ||| : | ||| ||:||:||||:|:||||||:||::|
Db   894 PKPIRRRCNQHPCSQPVVWTEEWGACSRSCGKLGVQTR---GIQCLLPLSNGTHKVMPA 949

Qy    66 EADLEENIKKGKKCIRTPKISKPIKFEL----SGCTSMKTYRAKFCG------------- 108
                      ::    |::    |  | :::::||:||||   |
Db   950 KACAGDRPEARRPCLRVP---CPAQWRLGAWSQCSAT-------CGEGIQORQVVCRTNA 999

Qy   109 -------------VCTDGRCCTPHRTTLPV---EFKCPDGEVMKKN--MMFIKTCAC 148
                          :||:  | :: | | ||
Db  1000 NSLGHCEGDRPDTVQVCSLPACGGNHQNSTVRADVWELGTPEGQWVPQSGPLHPINKISS 1059

Qy   149 HYNCPGDNDIF 159
            ||:||||
Db  1060 TEPCTGDRSVF 1070
```

RESULT 14
US-11-039-398-18
; Sequence 18, Application US/11039398
; Publication No. US20050267297A1
; GENERAL INFORMATION:
; APPLICANT: Friddle, Carl Johan
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Walke, D. Wade
; APPLICANT: Hilbun, Erin
; APPLICANT: Nepomnichy, Boris
; APPLICANT: Hu, Yi
; TITLE OF INVENTION: Novel Human Proteases and
; TITLE OF INVENTION: Polynucleotides Encoding the Same
; FILE REFERENCE: LEX-0221-USA
; CURRENT APPLICATION NUMBER: US/11/039,398
; CURRENT FILING DATE: 2005-01-20
; PRIOR APPLICATION NUMBER: US/09/938,330
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: US 60/227,104
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: US 60/233,796
; PRIOR FILING DATE: 2000-09-19
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 1232

```
;       TYPE: PRT
;       ORGANISM: homo sapiens
US-11-039-398-18

Query Match    10.7%;  Score 102;  DB 7;  Length 1232;
Best Local Similarity  22.0%;  Pred. No. 0.0088;
Matches  42;  Conservative  27;  Mismatches  62;  Indels  60;  Gaps  9;

Qy     15 PTMIRANC-------LVQTTEWSACSKTCG-MGISTRVTNDNASCRLEKQSRLCMVRPC 65
                      |||||:|    |||  :|  : ||  |  :|:   :  |    ::  |
Db    894 PKPIRRCNQHPCSQPVWVTEEWGACSRSCGKLGVQTR----GIQCLLPLSNGTHKVMPA 949

Qy     66 EADLEENIKGKKCIRTPKISKPIKFEL---SGCTSMKTYRAKFCG-------------- 108
             : |: |||  ||: | :  :        |:|  |: ::  :||
Db    950 KACAGDRPEARRPCLRVP---CPAQWRLGAWSQCSAT-------CCGEGIQQRQVVCRTNA 999

Qy    109 ------------VCTDGRCCTPHRTTLPV---EFKCPDGEVMKKN--MMFIKTCAC 148
                      :|:| : ::|:  :   :: |  :  : ::     :
Db   1000 NSLGHCEGDRPDTVQVCSLPACGGNHQNSTVRADVWELGTPEGQWVPQSGPLHPINKISS 1059

Qy    149 HYNCPGDNDIF 159
          | ||  |  :|
Db   1060 TEPCTGDRSVF 1070


RESULT 15
US-11-039-398-22
Sequence 22, Application US/11039398
Publication No. US20050267297A1
GENERAL INFORMATION:
    APPLICANT: Friddle, Carl Johan
    APPLICANT: Turner, C. Alexander Jr.
    APPLICANT: Walke, D. Wade
    APPLICANT: Hilbun, Erin
    APPLICANT: Neponmichy, Boris
    APPLICANT: Hu, Yi
    TITLE OF INVENTION: Novel Human Proteases and
    TITLE OF INVENTION: Polynucleotides Encoding the Same
    FILE REFERENCE: LEX-0221-USA
    CURRENT APPLICATION NUMBER: US/11/039,398
    CURRENT FILING DATE: 2005-01-20
    PRIOR APPLICATION NUMBER: US/09/938,330
    PRIOR FILING DATE: 2001-08-22
    PRIOR APPLICATION NUMBER: US 60/227,104
    PRIOR FILING DATE: 2000-08-22
    PRIOR APPLICATION NUMBER: US 60/233,796
    PRIOR FILING DATE: 2000-09-19
    NUMBER OF SEQ ID NOS: 26
    SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 22
    LENGTH: 1249
    TYPE: PRT
    ORGANISM: homo sapiens
US-11-039-398-22

Query Match    10.7%;  Score 102;  DB 7;  Length 1249;
Best Local Similarity  22.0%;  Pred. No. 0.0089;
Matches  42;  Conservative  27;  Mismatches  62;  Indels  60;  Gaps  9;

Qy     15 PTMIRANC-------LVQTTEWSACSKTCG-MGISTRVTNDNASCRLEKQSRLCMVRPC 65
                      |||||:|    |||  :|  : ||  |  :|:   :  |    ::  |
Db    894 PKPIRRCNQHPCSQPVWVTEEWGACSRSCGKLGVQTR----GIQCLLPLSNGTHKVMPA 949

Qy     66 EADLEENIKGKKCIRTPKISKPIKFEL---SGCTSMKTYRAKFCG--------------- 108
             : |: |||  ||: | :  :        |:|  |: ::  :||
Db    950 KACAGDRPEARRPCLRVP---CPAQWRLGAWSQCSAT-------CCGEGIQQRQVVCRTNA 999

Qy    109 ------------VCTDGRCCTPHRTTLPV---EFKCPDGEVMKKN--MMFIKTCAC 148
                      :|:| : ::|:  :   :: |  :  : ::     :
Db   1000 NSLGHCEGDRPDTVQVCSLPACGGNHQNSTVRADVWELGTPEGQWVPQSGPLHPINKISS 1059

Qy    149 HYNCPGDNDIF 159
          | ||  |  :|
Db   1060 TEPCTGDRSVF 1070
```